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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 05-01-03
Searcher: Beverly @ 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site	Vendors
<input type="checkbox"/> STIC	<input type="checkbox"/> IG Suite
<input type="checkbox"/> CM-1	<input type="checkbox"/> STN
<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
<input type="checkbox"/> Type of Search	<input type="checkbox"/> APS
<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
<input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>CGN</u>

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run On: April 30, 2003, 13:02:10 ; Search time 2934 Seconds
(without alignments)
15563.157 Million cell updates/sec

Title: US-09-918-026A-3
Perfect score: 1569
Sequence: 1 atggagccaggcggggcccgcg.....cttggtctgccatacctag 1569

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1569	100.0	1569	9	AF099031	AF099031 Homo sapi
2	1564.2	99.7	2040	9	AF059203	AF059203 Homo sapi
3	1459	93.0	2078	9	AF053234	AF053234 Chlorocob
4	1129.6	72.0	1933	10	AB075946	AB075946 Rattus no
5	1115	71.1	2170	10	BC025931	BC025931 Mus muscu
6	1112.4	70.9	1607	10	AF078751	AF078751 Mus muscu
7	421.4	26.9	3041	10	S81092	S81092 acyl-coenzy
8	421.4	26.9	3697	10	MUSACACT	L42293 Mus musculu
9	412.2	26.3	1750	10	D86373	D86373 Rattus norv
10	410.4	26.2	1673	9	AF053336	AF053336 Chlorocob
11	407.2	26.0	4011	9	HUMACYLCOA	L21934 Homo sapien
12	406.4	25.9	3024	10	CGU47320	U47320 Crictetus
13	405.8	25.9	1528	9	AF354622	AF354622 Gorilla g
14	405.6	25.9	3407	9	BC028940	BC028940 Homo sapi
15	405.6	25.9	4011	6	AR053912	AR053912 Sequence
16	405.6	25.9	4011	6	AR080271	AR080271 Sequence
17	405.6	25.9	4011	6	II17130	II17130 Sequence 3
18	404	25.7	1672	9	AF053337	AF053337 Macaca fa
19	404	25.7	2746	9	AK026611	AK026611 Homo sapi
20	404	25.7	3425	9	HS804938	AL833625 Homo sapi
21	402.8	25.7	1528	9	AF354623	AF354623 Pongo pyg
22	359.8	22.9	4079	6	AR053911	AR053911 Sequence
23	359.8	22.9	4079	6	AR080270	AR080270 Sequence
24	359.8	22.9	4079	6	II17129	II17129 Sequence 2
25	268.2	17.1	295	9	F331502S06	F331502S06
26	268.2	17.1	11317	9	AF332857S2	AF332857 Homo sapi
27	268.2	17.1	81364	2	AC021072_3	AC021072_3
28	268.2	17.1	157807	9	AC073573	AC073573 Homo sapi
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31	173.8	11.1	163811	2	AC110347	AC110347 Rattus no
32	172	11.0	74310	2	AC013041	AC013041 Drosophil
33	172	11.0	167467	3	AC009512	AC009512 Drosophil
34	172	11.0	186322	3	AC008314	AC008314 Drosophil
35	172	11.0	242566	3	AE003680	AE003680 Drosophil
36	171	10.9	2102	3	AY113537	AY113537 Drosophil
37	169	10.8	156297	2	AC123791	AC123791 Mus muscu
38	150.4	9.6	176	9	F331502S14	F331502S14
39	142.6	9.1	181870	2	AC024216	AC024216 Homo sapi
40	140.4	8.9	177	9	F331502S03	F331502S03
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43	135	8.6	170	9	F331502S10	F331502S10
44	134.6	8.6	996	6	AR053910	AR053910 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA,
complete cds.
ACCESSION AF099031
VERSION AF099031.2 GI:4878036
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Chang,C.C., Sakashita,N., Ornvold,K., Lee,O., Chang,E.T., Dong,R.,
Lin,S., Lee,C.Y., Strom,S.C., Kashyap,R., Fung,J.J., Farese,R.V.

Jr., Patoisseau, J.F., Delhon, A. and Chang, T.Y.
Immunological quantitation and localization of ACAT-1 and ACAT-2 in
human liver and small intestine
J. Biol. Chem. 275 (36), 28083-28092 (2000)
20428724
PUBMED
10846185
REFERENCE
2 (bases 1 to 1569)
Lee, O., Farese, R.V. Jr. and Chang, T.Y.
Human ACAT-2 nucleotide sequence
Unpublished
JOURNAL
3 (bases 1 to 1569)
Lee, O., Farese, R.V. Jr. and Chang, T.Y.
Direct Submission
Submitted (15-OCT-1998) Biochemistry, Dartmouth, HB 7200, Hanover,
NH 03755, USA
REFERENCE
4 (bases 1 to 1569)
Lee, O., Farese, R.V. Jr. and Chang, T.Y.
Direct Submission
Submitted (20-MAY-1999) Biochemistry, Dartmouth, HB 7200, Hanover,
NH 03755, USA
REMARK
Sequence update by submitter
COMMENT
On May 20, 1999 this sequence version replaced gi:3892234.
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BASE COUNT 276 a 473 c 453 g 367 t
ORIGIN

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DB 1 ATGGAGCCAGGGCGGCGGCTGCTGCTGAGAGACAGAGGCTGGGAGGGAGCGG 60
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ORIGIN									
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Best Local Similarity	95.8%	Prod. No.	9_9e-282;						
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QY	301	CAGA	AAGT	TTTT	CATCATCCGCAAGTCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTTC	360			
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QY	361	CGC	ACAT	CTAC	CACATGTTTCATCGCTGGCTGTGTCCTTCATCATCAGCACCCCTGGCC	420			
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```

2 (bases 1 to 1933)
Yukio, F., Katsunori, M. and Takeshi, O.
Direct Submission
Submitted (11-DEC-2001) Furuichi Yukio, Mie University,
Biorepositories: Kamihama, Tsu, Mie prefecture 514-8507, Japan
(E-mail: furuichi@bio.mie-u.ac.jp, Tel: 81-59-231-9612,
Fax: 81-59-231-9684)
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BASE COUNT 407 a 565 c 517 g 444 t

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	QY	DB	QY	QY	DB
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RESULT 5	
BC025931	
LOCUS	2170 bp mRNA linear ROD 07-AUG-2002
DEFINITION	Mus musculus, Similar to sterol O-acetyltransferase 2, clone MGC:36039 IMAGE:5099063, mRNA, complete cds.
ACCESSION	BC025931
VERSION	BC025931.1 GI:19884141
KEYWORDS	MGC.

Qy	145	AAGGCACAATTTGCTGGAGCAACGCCAGGACAATGAGGGAGCTGCTGGATTCGGGCCATG	204
Db	201	AAGACACAGTTTCTGGAGCAACACAGAGAGAGTTGGCAGAGCTGTTGGATTCGGGCCCTA	260
Qy	205	CGGAGGCTATACAACTCTACCCTACAAAGACAAACCTCTGCCCCACACCTCCCCCAAGGT	264
Db	261	TGGAGGCTATGCMAGCTTACCCCAACACAGACACCTCTTCCTCGCTGCCCGCCAGAT	320
Qy	265	TCCTTGAGCAGCACCCAGGAGCCATCCCTGGGGAAACAGAAAGTTTTCATCATCCGCAAG	324
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Qy	325	TCCCTGCTTGATGAGCTGATGAGGTGCAGCATTTCCGCAACCATCTACCCACATGTTTCATC	384
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Qy	385	GCTGGCCTGTGTCTTCAATCATCAGCACCTTGGCCATCTGACTTCATTTGATGAGGGCAGG	444
Db	441	GCGGGCTATGGCTCTGATCATGACACCCCTGGCCATCGACTTCATGATGAGGCGAG	500
Qy	445	CTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTTCGGACAGCTGCCATTTGGCGCTGGTG	504
Db	501	TTGATGCTGGAGTTTGACTTTACTCTCTTCAGCTTCGGACAGCTGCCCTTGGCGCTGATG	560
Qy	505	ACCTGGGTGCCATGTTTCTGTGTCACACCTGTTGGCGCGTACCAGGCCCTACGGCTGTGG	564
Db	561	ACCTGGGTTCCCATGTTCTGTCTACGCTCTAGTGGCCCTACCAAGACCCCTGTGGCTGTGG	620
Qy	565	GCCA-----GGGGCACCTTGAGCGGACGCGCGGCTTGGGCTGTGGCTTTTGA	612
Db	621	GCCAGCGCGCGCTGGGGGTGCCGTGATGCTGGGGGCCAGCTTGGCTGCTGCTG	680
Qy	613	GC CGCCACGCGGTGTGCTGTGCGCGCTGCGGGTCAAGTGGCCGTGGAGCATCAGCTC	672
Db	681	GCTGCCACGCTGTGGTGTCTGCTGCTGCGGTGTCAGTGTGTCAGTGAAGCATAGACTT	740
Qy	673	CCCGCGGCTCCCGTTGTCTGTCTTCGAGCAGGTTAGTTCCTTGATGAAAAGCTAC	732
Db	741	CCCGCGGCTCGGCTGCTGTGTCTTTGAGCAGGTCAGATTCGTGATGAAAAGCTAC	800
Qy	733	TCCTTCTTGAGAGAGGCTGTGCTGGGATCTCTGTGTCGACAGAGGTGAGGGGATCCAG	792
Db	801	TCCTTCTTGAGAGAGACTGTGCTGGGATCTTTTGTGCAGAGGAGAAAGGCGATCAGC	860
Qy	793	GCCCCAGTTTCTCCAGCTTACCTCTACTTCTCTGCCCAACATCATCTACAGGGAG	852
Db	861	CCCCCAAGTTTCTCCAGCTTACCTCTACTTCTCTGCCCTACACTTATCTACAGAG	920
Qy	853	ACTTACCCTAGGACGCCCTATGTCAGGTGGAAATATGTGGCAAGAACTTTGCCACGGCC	912
Db	921	ACATACCCAGGACCCAGCATCAGTGGAACTATGTGGCAGAACTTTGCCAGGTC	980
Qy	913	CTGGGATGTGTCTATGCCCTTCATCTCTGGGCCGCCCTCTGTGTCTGTCTTTGGC	972
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Db	1041	AACATGAGCGGGAACCCCTTCAGCACCGGGGCTCTGTGTCTCTCCATCTTGCATGCCACG	1100
Qy	1033	TTGCCAGGATCTTTCATGCTGTGTCTATCTTCTTTGGCTTCTTCCCAATGCTGGCTCAAC	1092
Db	1101	GGGCCAGGCATTTTCATGCTGCTCTCATCTTCTTCGGCTTCTCTGCATGCTGGCTCAAC	1160
Qy	1093	GCCTTTGCCGAGATGCTACGATTTTGGAGACAGGATGTTTCTACCGGGACTGGTGGAACTCA	1152
Db	1161	GCCTTGCCCGAGATGCTGCGGTTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCG	1220
Qy	1153	ACGTCTCTTCCAACTACTACCGCACTTGGAAAGCTGGTGGTTCATGACTGGCTGTACAGC	1212
Db	1221	ACTTCTCTTCCAACCTACTACCGCACTTGGAAAGCTGGTGGTTCATGACTGGCTGTACAGC	1280

Qy	1213	TACGTGTATCAGGATGGCTCGGCTCTTGCTGCCCGGGCCAGGAGGTAGCCATCGT	1272
Db	1281	TATGTGTATCAAGATGGGCTGTGCTTATAGGAGGCGGGCTCGCGGGTGGCCATCGT	1340
Qy	1273	GGTGTGTTCCCTGGGCTCCGCAAGTGGCCCATCAGTATATCTTCTGCTTCGCTCGGCTTC	1332
Db	1341	GGAGTGTTCCTTGGTCTCTGCGGTGGTTCATCAGTATATCTTCTGCTTCGCTCGGCTTC	1400
Qy	1333	TTCTATCCCGTCATGCTGATATCTTCTCTTCTCATTTGGAGGAATGTTGAACCTTCATGATG	1392
Db	1401	TTCTATCCCGGTATGCTGATCTATCTTCTCTTCTTGGGGGGCTGCTGAATTTCCACATG	1460
Qy	1393	CATGACACAGCCACCGCGCCGCTGGAACCTGCTGATGTGAGCACATCTCTCTTCTTAGGC	1452
Db	1461	AACGACAGGCACAGGTCACGCTGGACATCTGATGTGAGCATCTTCTCTTCATGGGC	1520
Qy	1453	CAGGGAATCCAGGTCAGCCTCTACTGCCAGAGTGGTACGACACGCGGCACACTGCCCTTA	1512
Db	1521	CAGGCAATCCAGGTCAGCCTTACTGCCAGAGTGGTATGCTGCTCGACACTGTCCCTG	1580
Qy	1513	CCCGAGCAACTTCTTGGGGCTGGTGACACCTCGATCTTGGTCTTCCCATACCTAG	1569
Db	1581	CCCGAGCAACTTCTTGGGGGATGCTGACACCCGCTCTTGGTCTGCTGCACTCCCTAG	1637
RESULT 6.			
AF078751			
LOCUS: 1607 bp mRNA linear ROD 15-OCT-1998			
DEFINITION Mus musculus acyl coenzyme A:cholesterol acyltransferase-2			
(Acact-2) mRNA, complete cds.			
ACCESSION AF078751			
VERSION AF078751.1 GI:3746693			
KEYWORDS Mus musculus.			
SOURCE Mus musculus			
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;			
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Cases,S., Novak,S., Zheng,Y.W., Myers,H.M., Lear,S.R., Sande,E.,			
Welch,C.B., Lusis,A.J., Spencer,T.A., Krause,B.R., Erickson,S.K.			
and Farese,R.V. Jr.			
ACAT-2, a second mammalian acyl-CoA:cholesterol acyltransferase.			
Its cloning, expression, and characterization			
J. Biol. Chem. 273 (41), 26755-26764 (1998)			
REFERENCE 98434591			
PUBMED 9756919			
REFERENCE 2 (bases 1 to 1607)			
Farese,R.V. Jr.			
Direct Submission			
AUTHORS Submitted (16-JUL-1998) Gladstone Institute, 2550 23rd Street, San			
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BASE COUNT	299 a	466 c	456 g	385 t	1 others
ORIGIN					

Query Match	70.9%;	Score 1112.4;	DB 10;	Length 1607;
Best Local Similarity	83.2%;	Pred. No. 2.2e-212;		
Matches 1295; Conservative	0;	Mismatches 247;	Indels 15;	Gaps 2;

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Qy	85	AAACCTGAGACGCACAGAGCCCGGACTTGGTACAAATGACACCGACACATGAGGCTGTG	144	
Db	111	AACGCAGGACACACGAAACCCAGACTTGGTGCATGGACTCGACATATGAGGCTGTG	170	
Qy	145	AAGCGCAATTTGCTGAGCAGAGCGCAGGAGCAACTGACGAGGAGCTGCTGATCGGCCCCATG	204	
Db	171	AAGACNCAGTTTCTGGAGCAAGCACAGAGAGAGTTGGCAGAGACTGTGATCGGGCCCTTA	230	
Qy	205	CGGAGGCTATACAATCTTACCCATCACAAAGACAAAACCTCTGCCCCACACTCCCCAGGT	264	
Db	231	TGGAGGCTATGACAGTTTACCCCAACACAGACAGACTTCTCCCTCCGCTGCCCCAGAT	290	
Qy	265	TCCTTTGAGCAGGACCCAGGAGCATTCCCTGGGGAAACAGAAAGTTTTCATCATCTCCGCAAG	324	
Db	291	TCACAAAGAACCCCGGAGTTACGCCCTGGAAAAAGAAAGTTTTCGCTCGCCCGCAAG	350	
Qy	325	TCCTTGCTTCATGAGCTGATGGAGGTGCAGCATTTCCGACACATCTACACATGTTTCATC	384	
Db	351	TCACTGATCATGAGCTAATGAGAGGTGCACATTTCCGAACCATCTACACATGTTTCATA	410	
Qy	385	GCTGGCCTGTGTCTTCATCATCAGCACCCCTGCCCATCGACTTCATTGATGAGGCGAG	444	
Db	411	CGGGCCCTATGGTCTTTGATCATCAGCACCCCTGCCCATCGACTTCATTGATGAGGCGAG	470	
Qy	445	CTGCTCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTTGGGCGTGGTG	504	
Db	471	TTGATGCTGGAGTTTGACTTACTCTTTCAGCTTCGGACAGCTGCCCTTGGCGCTGATG	530	
Qy	505	ACCTGGGTGCCCATGTTTCTCTCCACCCTGTTGCGCCGTACCAGAGCCCTACGGCTGTGG	564	
Db	531	ACCTGGGTGCCCATGTTTCTCTATACGCTCCTAGTGGCCTTACCAGACCCCTGTGGCTGTGG	590	
Qy	565	GCCA-----GGGGCACTTGACACAGCGCACGGCCCTGGGGCTGTGGCGCTTTTA	612	
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Qy	613	GCCGCCACAGCGGTGTGCTCTGGCGCCTGCGGTCACGCTGGCGCTGGAGCATCAGCTC	672	
Db	651	GCTGCCACGCTGTGTGTCTCTGGCTCTTCCCGGTCACGCTGTGAGGCACTGAGCTT	710	
Qy	673	CCGCCGCTCCCTGTGTGCTTCTGACGAGGTTAGGTTCTGATGAAAGCTAC	732	
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Qy	733	TCCTTCCTGAGAGGCTGTGCCTGGGATCTTCTGTCACAGAGAGTGTAGGGGATCCAG	792	
Db	771	TCCTTCCTGAGAGACTGTGCCTGGGATCTTTTGTGTACAGAGGAGAAAGGCATCAGC	830	
Qy	793	GCCGCCAGTTTCTCCAGTACTCTACTTCTCTTCTGCCCCAACACTCATCTACAGGAG	852	
Db	831	CCCCAAGTTTCTCCAGCTACTCTACTTCTCTCTGCCCCAACACTTATCTACAGAGAG	890	
Qy	853	ACTTACCCTAGGAGCCCTATGTCAGGTGGAATATCTGGCCCAAGAACTTTGCCAGGCC	912	
Db	891	ACATACCCCAAGGACACCCAGCATCAGGTGGAACTATGTGGCCCAAGAACTTTGCCAGGTC	950	
Qy	913	CTGGGATGTGTGCTCTATGCGCTGCTTCATCTCGGGCGCCCTGTGTTCTCTGCTTTGCC	972	

Db	951	CTGGGCTGTTTGGCTCTATGCGTCTTCATCCTGGCGCGCTCTGTGTCCTGCTCTTGGC	1011
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Qy	1033	TTGCCAGGACATTTCATGCTGTGTCTCATCTTCTTTGGCTTCTCTCATTTGCTTGGCTCAAC	1092
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Qy	1093	GCCTTTGCCAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCA	1152
Db	1131	GCCTTCGCCAGATGCTGGGTTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCG	1190
Qy	1153	ACGTCCTCTTCCAACCTACTACCGCACTTTGGAACGCTGGTGTCATGACTGGCTGTACAGC	1212
Db	1191	ACTTCCTTCTCCAACCTACTACCGCACTTGGAAAGCTGGTGTCATGACTGGCTGTACAGC	1250
Qy	1213	TACGTGTATCAGGATGGCTGGCGTCTCTTGGTGCCCGGGGCCGAGGGGTAGCCATGCTG	1272
Db	1251	TATGTGTATCAAGATGGCTGGTCTTTAGGACAGCGGGCTCGGGGTGGCCATGCTG	1310
Qy	1273	GGTGTGTCTCGTCTCCGACGTGGCCATGAGTATATCTTCTGCTCTGCTCCTGGGGTTC	1332
Db	1311	GGAGTGTCTCGTGTCTCGGGTGGTTTCATGAGTATATCTTCTGCTCTCGCTGGGGTTC	1370
Qy	1333	TTCTATCCCGTCACTGATGACTCTTCTCTTGTCTATTTGGAGGAATGTTGAACCTCATGATG	1392
Db	1371	TTCTATCCCGTCACTGATGACTATTCCTTGTCTTTTCGGGGGGCTGCTGAATTTCCACCATG	1430
Qy	1393	CATGACAGCGCACCGCCGGCGATGGAACTGCTGATGTGGACCATGCTGTTTCTTAGGC	1452
Db	1431	AACGACAGGCACACAGGCTCCAGCTTGGAACTTCCTGATGTGGAACTTCTCTTCATGGGC	1490
Qy	1453	CAGGGAATCCAGTTCAGCTGTACTGCCAGGAGTGGTAGCGACAGCGCGCACTGCCCCCTTA	1512
Db	1491	CAGGGCATCCAGTTCAGCTATCTACTGCCAGGAGTGGTAGCTGTCGACACTGTCCCTGT	1550
Qy	1513	CCCCAGGCAACTTCTGGGGGCTGGTGACACCTCGCATCTTGGTCTCTGCGCATACCTAG	1569
Db	1551	CCCCAGCAACATTTCTGGGGATGGTGACACCCCAATCTTGGTCTCTGCGCATACCTAG	1607

REF: T 7

LOCUS	S81092	3041 bp	linear	ROD 03-AUG-1996
DEFINITION	acyl-coenzyme A:cholesterol acyltransferase [mice, peritoneal macrophages. mRNA, 3041 nt].			

ACCESSION	S61092
VERSION	S81092.1
	GI:1478335

KEYWORDS . Mus sp. peritoneal macrophages.
SOURCE

SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE 1 (bases 1 to 304)

AUTHORS Green, S., Steinberg, D. and Quehenberger, O.
TITLE Cloning and expression in Xenopus oocytes of a mouse homologue of the human acylcoenzyme A: cholesterol acyltransferase and its potential role in metabolism of oxidized LDL

JOURNAL OF BIOCHEMICAL PHYSIOLOGY 218 (3), 924-929 (1996)

JOURNAL
MEDLINE
96158986

RECEIVED
PURBMD 8579615

REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI accession 175976] from the original journal article.
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FEATURES

FEATURES

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gene 3041

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573	QY	----CACCTTGGAGCGAGGCGGCGCTGTGCCCTTTTAGCCGCCACACGCGTGG	628
756	Db	CTACCCTATGTACTATTCCTTGTCCATGGGCTTGCTCTTCTAGTCTTTCAACTTGGAG	815
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816	Db	TTCTAGGTTTGTGCCAACATAGTTGTCTTAGCATACACACTGCCACCACCTCCCGGT	875
689	QY	GTGTCCTGTCTTCGAGCAGGTAGGTTCTTGATGAAAGCTACTCTTCTCTGAGAGAGG	748
876	Db	TCATTCTGATCTGGAACAGATTCGTTTGTAAATGAAGGCTCACTCATTTGTCGAGAGA	935
749	QY	CTGTGCTCGGATCCTCTGTCGCACAGCAGGTGAGGGGATCCAGGCC-----CCAGTT	802
936	Db	ATATCCACAGTACTAAATGACGACGAGGAATCAAGCAAAAGATCCCATACCCACAG	995
803	QY	TCCTCCAGCTACCTACTCTCTCTCTGCCCCAACACTCATCTACAGGGAGACTTACCCTA	862
996	Db	TCAACAGTACCTGTACTTCTCTGTTGGCGCTACACTATTTACCGAGACAACATACC	1055
863	QY	GGAGCCCTATGTCAGGTGGAAATTTATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGTG	922
1056	Db	GGACTCTCTACTGTAAGATGGGTTATGTGCTATGCGCTATGCAAGTTTTTACAGAGTGT	1115
923	QY	TGCTCTATGCTCTCATCTCGGGCGGCTCTGTGTTCTCTGCTTTGCCAACATGAGCC	982
1116	Db	TGTTTATGTGTACTACATCTTTGAGAGACTCTGTGCCCACTATTCGCGAATATCAAC	1175
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ORIGIN

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DB 2380 CATTTCTGGATTATGTCGCGCGCGGACCTGGACTTGTCT 2418
RESULT 9
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DEFINITION Rattus norvegicus mRNA for acyl-coenzyme A:cholesterol
acyltransferase, complete cds.
ACCESSION D86373
VERSION D86373.1 GI:3036904
KEYWORDS acyl-coenzyme A:cholesterol acyltransferase.
SOURCE Rattus norvegicus (strain:Wistar) male adrenal grand cDNA to mRNA.
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (sites)
AUTHORS Matsuda,H., Hakamata,H., Kawasaki,T., Sakashita,N., Miyazaki,A.,
Takahashi,K., Shichiri,M. and Horiuchi,S.
TITLE Molecular cloning, functional expression and tissue distribution of
rat acyl-coenzyme A:cholesterol acyltransferase
JOURNAL Biochim. Biophys. Acta 1391 (2), 193-203 (1998)
MEDLINE 98223432
REFERENCE 2 (bases 1 to 1750)
AUTHORS Horiuchi,S.
TITLE Direct Submission

JOURNAL Submitted (04-JUL-1996) Seikoh Horiuchi, Kumamoto University School of Medicine, Department of Biochemistry; Honjo 2-2-1, Kumamoto, Kumamoto 860-0811, Japan (E-mail: horiuchi@jpo.kumamoto-u.ac.jp, Tel: 81-96-373-5088, Fax: 81-96-364-6940)

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ACCESSION AF053336
VERSION AF053336.1
KEYWORDS mRNA, complete cds.
SOURCE Cercothecus aethiops.
ORGANISM Cercothecus aethiops.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheciae; Cercopithecus.
REFERENCE 1 (bases 1 to 1673)
AUTHORS Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M.,
Shelness, G.S. and Rudel, L.L.
TITLE Identification of a form of acyl-CoA:cholesterol acyltransferase
specific to liver and intestine in nonhuman primates
J. Biol. Chem. 273 (41), 26747-26754 (1998)
PUBMED 9756918
REFERENCE 2 (bases 1 to 1673)
AUTHORS Anderson, R.A., Joyce, C., Davis, M., Reagan, J., Clark, M., Shelness, G.
and Rudel, L.L.

TITLE Direct Submission
 JOURNAL Submitted (11-MAR-1998) Internal Medicine, Wake Forest University
 School of Medicine, Medical Center Boulevard, Winston-Salem, NC
 27157, USA

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BASE COUNT 405 a 359 c 359 g 550 t
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 Best Local Similarity 59.11; Pred. No. 6e-72;
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 REFERENCE
 1 (bases 1 to 4011)
 AUTHORS Chang,C.C., Huh,H.Y., Cadigan,K.M. and Chang,T.Y.
 TITLE Molecular cloning and functional expression of human acyl-coenzyme
 A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovary
 cells
 JOURNAL J. Biol. Chem. 268 (28), 20747-20755 (1993)
 MEDLINE 94012607

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AUTHORS
TITLE
JOURNAL
SUBMITTED (02-NOV-1993) Biochemistry Dept, Dartmouth Medical School, Hanover, NH 03755, USA
3 (bases 1 to 4011)
Chang, C.C. and Chang, T.Y.
Direct Submission
JOURNAL
TITLE
JOURNAL
SUBMITTED (20-MAY-1999) Biochemistry Dept, Dartmouth Medical School, Hanover, NH 03755, USA
Sequence update by submitter
On May 20, 1999 this sequence version replaced gi:409203.
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

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Hedges, S.B.
Human and ape molecular clocks and constraints on paleontological hypotheses
J. Hered. 92 (6), 469-474 (2001)
MEDLINE 21945518
PUBMED 11948213
REFERENCE 2 (bases 1 to 1528)
AUTHORS Hedges, S.B.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Department of Biology, The Pennsylvania State University, 208 Mueller Lab, University Park, PA 16802, USA
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DB 1521 ACATTTT 1527
RESULT 14
BC028940
LOCUS
DEFINITION
Homo sapiens, sterol O-acyltransferase (acyl-Coenzyme A:
cholesterol acyltransferase) 1, clone MGC:29940 IMAGE:4991365,
mRNA, complete cds.
ACCESSION
BC028940
VERSION
BC028940.1 GI:20809439
KEYWORDS
MGC.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3407)
AUTHORS
Strausberg, R.
TITLE
Direct Submission

JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 42 Row: 1 Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

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BASE COUNT 940 a 628 c 681 g 1158 t
ORIGIN

Query Match 25.9%; Score 405.6; DB 9; Length 3407;
Best Local Similarity 58.9%; Pred. No. 5.1e-71;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;
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DB 404 CACCTCCAGAACAGGAAGATTTTATTTGCAAGCGCTCTCTCTAGTAGACTGCTTG 463
QY 347 AGGTGACAGATTTCGCCACCATCTACACATGTTTCATCGCTGGCTGGCTGTGTTTCATCA 406
DB 464 AAGTGGACCATCAGAACAAATATACATGTTTATTGCCCTCCTCATCTCTTTATCC 523
QY 407 TCAGCACCTTGGCCATCGACTTCATGATGAGCGAGGCTGCTGCTGGAGTTTGACCTAC 466
DB 524 TCAGCACCTTGTAGTAGATTCATGATGAGGAGGCGTGGTGTCTGAGTTGACCTCC 583
QY 467 TGATCTTACGCTTCGGACAGCTGCCATGTCGCTGGTGGCTGGTGGCTGGCTGGCTGGCT 526
DB 584 TGCTTATGCTTTGGCAATTTCTTACCTACCTGTTGTTGGACCTGGTGGATCATGTTCTGT 643

QY 527 CCACCTGTTGGCGGTACACAGCCCTACGGCTGTGGGCCACAGGGCCACTGGACGAGG 586
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QY 587 CGACGGGCTGGGCTGTGGCTTTTAGCGGCCACAGCGGCTGTGCTGTGCGCGCTGCCG 646
DB 704 CTCATCGGCTGATCGGTTCTCTCTTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG 763
QY 647 TCC-----ACGTGGCGGTGAGCATCAGCTCCCGCGGCTCCCGTT 688
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QY 862 AGGACGCCCTATGTCAGGTGGAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGT 921
DB 1003 AGGAATCCCACTGTAAGATGGGTTATGCTGTATGAAGTTTGACAGGTTCTTTGGTTGC 1062
QY 922 GTCTCTATGCTCTCTCTCTCTGCGGCCCTCTGTGTTCTCTCTTGTGCAACATGAGC 981
DB 1063 TTTTCTTATGTGTACTACATCTTTGAAAGCTTTTGGCCCTTTGTCGGAATATCATA 1122
QY 982 CGAGAGCCCTTCAGCACCCGCTGCTCTCTCTATCTATCTGATGCCAGTTGCCAGGC 1041
DB 1123 CAGGACCCCTTCAGGCTCGTCTGTTCTGCTATGTATTAATCACTCATCTTGGCAGGT 1182
QY 1042 ATCTTATGCTGTCTCTCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1101
DB 1183 GTCTGATTTCT 1242
QY 1102 GAGATGCTACGATTTGGACACAGATGTTCTACGGGACTGTTGGAACCTCAAGCTCTTC 1161
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QY 1162 TCCAACTACTACCGCACTTGGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
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DB 1603 TTAATCT 1662
QY 1522 ACTTCTTGGGGGCTGCTGACACCTCGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563
DB 1663 ACATTTTGGGATATGCTCCCGCCAGCTTCTCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCT 1704

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 12:17:55 ; Search time 262 Seconds
(without alignments)
13486.204 Million cell updates/sec

Title: US-09-918-026a-3

Perfect score: 1569

Sequence: 1 atggagccagcggggcccgcg.....cttggtctgcacacacacgtag 1569

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1564.2	99.7	2040	21	AA76170 Human ACAT Related
2	1425.8	90.9	1509	21	AA257360 Human acyl CoA:cho
3	1112.4	70.9	1607	21	AA257359 Mouse acyl CoA:cho
4	645	41.1	1082	19	AAV01534 Human acylcoenzyme
5	407.2	26.0	4011	15	AAQ63212 Acetyl coenzyme A:
6	404	25.7	3649	19	AAV01536 Human acylcoenzyme
7	394.6	25.1	3650	19	AAT96368 Human acyl-coenzym
8	191.8	12.2	455	19	AAV01545 Acylcoenzyme A:cho
9	172	11.0	1885	23	ABL13759 Drosophila melanog

10	172	11.0	2657	23	ABL15694	Drosophila melanog
11	172	11.0	4260	23	ABL13758	Drosophila melanog
12	134.6	8.6	996	15	AAQ63210	Acetyl coenzyme A:
13	95	6.1	983	19	AAV01539	Human acylcoenzyme
14	95	6.1	993	22	AAV06413	Human cDNA SEQ ID
15	95	6.1	1521	19	AAV01533	Human acylcoenzyme
16	95	6.1	1895	21	AA257359	Human acyl CoA:cho
17	95	6.1	1895	21	AA257359	DNA encoding a pro
18	95	6.1	1976	21	AA76169	Human ACAT Related
19	93.8	6.0	542	22	AA27552	cDNA encoding nove
20	92.4	5.9	774	22	AA27244	cDNA encoding nove
21	88.2	5.6	447	21	AA28517	Human secreted pro
22	81.4	5.2	452	24	ABL1686	Human ovarian can
23	81.4	5.2	1650	21	AA249452	Mouse Diacylglycer
24	80	5.1	1122	20	AA30335	DNA encoding a hum
25	79.8	5.1	1766	21	AA28846	Rat acyl CoA:chole
26	79.8	5.1	1766	21	AA25385	Acyl-CoA:cholester
27	79.8	5.1	1766	22	AA201105	Rat sterol acyltra
28	70.2	4.5	1559	21	AA48935	Corn diacylglycer
29	69.6	4.4	978	21	AA48934	Corn diacylglycer
30	69.6	4.4	1281	21	AA48933	Corn diacylglycer
31	65	4.1	901	21	AA48936	Corn diacylglycer
32	64.8	4.1	1587	21	AA48938	Rice diacylglycer
33	60.6	3.9	5574	24	AA563338	Chemically pretrea
34	60.4	3.8	1975	21	AA48942	Wheat diacylglycer
35	59	3.8	60	24	ABN36849	Human spliced tran
36	59	3.8	1942	21	AA48939	Soybean diacylglyc
37	55.4	3.6	4170	22	AAK69416	Human immune/haema
38	55.4	3.5	519	21	AA48843	M. alpina acyl CoA
39	55.4	3.5	519	21	AA245380	Acyl-CoA:cholester
40	55.4	3.5	519	22	AA201319	Mortierella alpina
41	52.8	3.4	10732	3.4	AA10594	Gene encoding a su
42	50	3.2	1888	21	AA48932	Arabidopsis diacyl
43	50	3.2	1904	21	AA51482	A. thaliana diacyl
44	50	3.2	1942	21	AA48835	Arabidopsis acyl C
45	50	3.2	1942	21	AA245371	Acyl-CoA:cholester

ALIGNMENTS

RESULT 1

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ID AA76170 standard; DNA: 2040 BP.

XX AC AA76170;

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XX AC AA76170;

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XX AC AA76170;

XX AC AA76170;

XX AC AA76170;

PI Sturley SL, Oelkers P;
 XX WPI: 2000-557622/51.
 DR P-PSDB; AAB21640.
 XX
 PT New nucleic acid encoding a human diacylglycerol acyltransferase,
 PT useful for treating hyperlipidemia, atherosclerosis, heart disease, or
 PT other diseases associated with an imbalance of triglyceride levels
 XX
 PS Disclosure; Fig 2B; 32pp; English.
 XX
 CC The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates
 CC sterol esterification, an important component of intracellular lipid
 CC homeostasis. The present sequence is the coding sequence of human ACAT
 CC Related Gene Product 2 (ARGP2/ ACAT2). The enzyme encoded by the present
 CC sequence is a diacylglycerol acyltransferase (DGAT). ARGP2 esterifies
 CC cholesterol. Also, the activity of ARGP2 is relatively resistant to
 CC histidine active site modifier. ARGP2 is therefore a tissue specific
 CC sterol esterification enzyme.
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 SQ Sequence 2040 BP; 389 A; 604 C; 577 G; 470 T; 0 other;
 Query Match 99.7%; Score 1564.2; DB 21; Length 2040;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 DB 232 AGGAGCTGTGATCGGGCCATCGGGAGGCTATACATCTTACCCATCACAAGACAAA 291
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 DB 352 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGATGAGCTGATGGAGTGCAGCATTTT 411
 QY 361 CGCACCATCTACCAATGTTTCATCGTGGCTGTGTCTTTCATCATCAGACCCCTGGCC 420
 DB 412 CGCACCATCTACCAATGTTTCATCGTGGCTGTGTCTTTCATCATCAGACCCCTGGCC 471
 QY 421 ATCGACTTCATGATGAGGCGAGGCTGCTGCTGAGTTTGACCTACTGATCTTCAGCTTC 480
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 DB 592 CCGTACAGGCGCTACGGCTGTGGCCAGGCGCACCTGGAGCAGGCGGCGGCTGGGC 651
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 DB 712 GAGCATCAGCTCCCGCGGCTCCCGTGTGTCTGTGCTTTCGAGCAGGTTAGTTCCTG 771

QY 721 ATGAAAGCTACTCTCTCTGAGAGAGCTGTGCTGGATCCTTCTGTCGAGAGAGGT 780
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 QY 781 GAGGGATCCAGGCCCCCAGTTTCTTCCAGCTACCTCTACTTCTCTCTCTCTCTCTCT 840
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 QY 841 ATCTACAGGAGACTTACCTTAGGACGCCCTATGTCAGTGGAAATATGTGCCAAGAAC 900
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 QY 1261 GTAGCCATGCTGGTGTGTCTCTGCTCTCGAGTGGCCCATGAGTATATCTTCTCTCTCT 1320
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 QY 1381 AACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 DB 1432 AACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1491
 QY 1441 CTGTTCTAGGCGCAGGAAATCCAGGTCAGCTCTACTTGGCAGGAGTGGTACGACGCGG 1500
 DB 1492 CTGTTCTAGGCGCAGGAAATCCAGGTCAGCTCTACTTGGCAGGAGTGGTACGACGCGG 1551
 QY 1501 CACTGCCCCCTTACCCAGGCAACTTCTTGGGGCTGTGTGACACTCGATCTTGGTCTCTGC 1560
 DB 1552 CACTGCCCCCTTACCCAGGCAACTTCTTGGGGCTGTGTGACACTCGATCTTGGTCTCTGC 1611
 QY 1561 CATACCTAG 1569
 DB 1612 CATACCTAG 1620

RESULT 2
 AA257360
 ID AA257360 standard; cDNA; 1509 BP.
 XX
 AC AA257360;
 XX AC
 DT 05-APR-2000 (first entry)
 XX
 DE Human acyl CoA:cholesterol acyltransferase 2 encoding cDNA.
 XX
 KW Human; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis;

KW antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;
KW hyperlipidaemia; ss.
OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..1509

XX /tag= a

XX /product= "ACAT-2"

XX /transl_except= (pos:571..573,aa:Xaa)

XX /note= "Xaa is unspecified"

XX W09967368-A1.

XX 29-DEC-1999.

XX 16-JUN-1999; 99WO-US13683.

XX 23-JUN-1999; 98US-0090354.

XX 08-JUN-1999; 98US-0328857.

XX (REGC) UNIV CALIFORNIA.

XX Cases S, Farese RV, Novak S, Erickson SK;

XX WPI; 2000-106291/09.

XX P-PSDB; AAY67953.

XX Novel polypeptide, useful to treat conditions associated with elevated
XX cholesterol ester levels e.g. hypercholesterolemia

XX Example; Page 52; 57pp; English.

XX The present sequence encodes the human acyl CoA:cholesterol
XX acyltransferase designated ACAT-2. ACAT-2 polypeptides can be
XX administered therapeutically, especially by expressing encoding
XX polynucleotides, to treat individuals in need of ACAT-2 polypeptide.
XX They may especially be administered to treat disease conditions
XX associated with elevated cholesterol ester levels e.g.
XX hypercholesterolaemia or hyperlipidaemia (including
XX hypertriglyceridaemia), since ACAT-2 catalyses the esterification of
XX cholesterol with fatty acyl CoA substrates. The polypeptides can also
XX be used to diagnose diseases related to polypeptide expression or
XX activity, by analysing for polypeptide presence or amount in a sample.
XX They are useful to screen for compounds inhibiting or activating the
XX polypeptide, which can be included in pharmaceutical compositions and
XX administered therapeutically to treat conditions associated with ACAT-2;
XX inhibitory agents can especially be used to inhibit ACAT-2 activity,
XX especially therapeutically, and especially agents which selectively
XX inhibit ACAT-2 and not prior art ACAT-1.

XX Sequence 1509 BP; 260 A; 457 C; 439 G; 351 T; 2 other;

Query Match 90.9%; Score 1425.8; DB 21; Length 1509;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1500; Conservative 0; Mismatches 9; Indels 60; Gaps 1;

QY 1 ATGGAGCCAGCGGGCCCGCTGCGCTGCGAGAGGACAGAGGGCTGGAGGGAGCGG 60

DB 1 ATGGAGCCAGCGGGCCCGCTGCGCTGCGAGAGGACAGAGGGCTGGAGGGAGCGG 60

QY 61 GAGCGCCAAACCTGTGGAGATGAACACTGAGACGACAGAGCCCGGACTTGGTACAA 120

DB 61 GAGCGCCAAACCTGTGGAGATGAACACTGAGACGACAGAGCCCGGACTTGGTACAA 120

QY 121 TGGACCCGACATGAGGCTGTGAGGACAAATTCCTGAGCAAGCGGAGGACAACTG 180

DB 121 TGGACCCGACATGAGGCTGTGAGGACAAATTCCTGAGCAAGCGGAGGACAACTG 180

QY 181 AGGGAGCTGCTGGATCGGGCCATGCGGGAGGCTATACAATCTTACCCATCACAAGACAA 240

DB 181 AGGGAGCTGCTGGATCGGGCCATGCGGGAGGCTATACAATCTTACCCATCACAAGACAA 240

QY 241 CCTCTGCCCCACCCTCCCCAGGTTCTTGGACGAGACCCAGGACCATCTCCTGGGAAA 300
DB 241 CCTCTGCCCCACCCTCCCCAGGTTCTTGGAGCAG----- 275
QY 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGGAGGTGAGCATTTTC 360
DB 276 -----TGAGCTGATGGAGGTGAGCATTTTC 300
QY 361 CGCACCATCTACACATGTTTCATCGCTGGCTGTGTCTTTCATCATCATGACACCTTGGCC 420
DB 301 CGCACCATCTACACATGTTTCATCGCTGGCTGTGTCTTTCATCATCATGACACCTTGGCC 360
QY 421 ATCGACTTCATTTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTACGTTTC 480
DB 361 ATCGACTTCATTTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTACGTTTC 420
QY 481 GGACAGCTGCCATTTGGCGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGG 540
DB 421 GGACAGCTGCCATTTGGCGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGG 480
QY 541 CCGTACCGAGGCTTACGGCTGTGGGCGAGGGCACCTGGACGACGAGCGGCGCTTGGG 600
DB 481 CCGTACCGAGGCTTACGGCTGTGGGCGAGGGCACCTGGACGACGAGCGGCGCTTGGG 540
QY 601 TGTGCGCTTTTAGCGCGCCACCGCGTGTGCTGTGCGCGCTGCCGCTCCAGCTGGCCGTG 660
DB 541 TGTGCGCTTGTAGCGCGCCACCGCGTGTGCTGTGCGCGCTGCCGCTCCAGCTGGCCGTG 600
QY 661 GAGCATCAGCTCCCGCGCGGCTCCCGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 601 GAGCATCAGCTCCCGCGCGGCTCCCGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 721 ATGAAAGCTACTCTCTCTGAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 661 ATGAAAGCTACTCTCTCTGAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 781 GAGGAGTCCAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 721 GAGGAGTCCAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 841 ATCTACAGGAGACTTACCTTAGGCGGCTATGTCAGGTGGAATATATGTGGCAGAAGAC 900
DB 781 ATCTACAGGAGACTTACCTTAGGCGGCTATGTCAGGTGGAATATATGTGGCAGAAGAC 840
QY 901 TTTGCCAGGCGGCTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 841 TTTGCCAGGCGGCTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 961 CTTGCTTTTGGCAACATGAGCGGAGAGCGGCTTACAGACCGGCTGCTGCTGCTGCTGCTATC 1020
DB 901 CTTGCTTTTGGCAACATGAGCGGAGAGCGGCTTACAGACCGGCTGCTGCTGCTGCTGCTATC 960
QY 1021 CTGATGCCAGCTTGGCAGGACATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 961 CTGATGCCAGCTTGGCAGGACATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1081 TGTGCTCTCAAGCGCTTTCCGAGAGTGTACGATTTTGAGACAGGATGTTTCTACCGGGAC 1140
DB 1021 TGTGCTCTCAAGCGCTTTCCGAGAGTGTACGATTTTGAGACAGGATGTTTCTACCGGGAC 1080
QY 1141 TGGTGAACCTAACGTCCTTCTCCAACTACTACCGGACCTTGGAACTGTTGGTGGTTCATGAC 1200
DB 1081 TGGTGAACCTAACGTCCTTCTCCAACTACTACCGGACCTTGGAACTGTTGGTGGTTCATGAC 1140
QY 1201 TGGCTCFACAGCTTACCTGTATCAGGATGGCTGCGGCTCCTTGGTCCCGGGCCCGAGGG 1260
DB 1141 TGGCTCFACAGCTTACCTGTATCAGGATGGCTGCGGCTCCTTGGTCCCGGGCCCGAGGG 1200
QY 1261 GTAGCCATGCTGGGTGTGTTCTTCCGAGTGGGCTTCCGAGTGGGCTATATCTTCTGCTTC 1320
DB 1201 GTAGCCATGCTGGGTGTGTTCTTCCGAGTGGGCTTCCGAGTGGGCTATATCTTCTGCTTC 1260
QY 1321 GTCTGGGGTCTTCTTATCCCGTATCCCGTATCCCGTATCCCGTATCCCGTATCCCGTATCC 1380

Db 2696 AAGGACTTTCTCTGGTTTTTCTCCAGAGATTCAAAATCTGCTGCCATGTTAGCTGCTTT 2755
Qy 1282 CTGGTCTCGGAGTGGCCCATGAGTATCTCTGCTCGCTCGCTGGGTTCTTCTATCC 1341
Db 2756 GCTGATCTGCTGATGACAGCAATATGCTTGGCTGTTGCTGAGCTTTTCTATCCC 2815
Qy 1342 GTGATGCTGATCTCTCTCTGCTGATGAGGAATGTTGAACCTTCATGATGATGACCC 1401
Db 2816 GTGCTGTGCTGCTCTCTGCTGATGAGGAATGTTGAACCTTCATGATGATGATGATG 2875
Qy 1402 CCCACGGCCCGGATGAGACGTGCTGATGAGCAATGCTTTCTAGGCCAGGGAATC 1461
Db 2876 CGGAAAAAGCCGATTTGGAATGTTGATGAGCAATGCTTTCTTTGCGCAATGGAGTC 2935
Qy 1462 CAGGTCAGGCTCTACTGCGCAGGAGTGGTACGACGCGGCACTGCCCCCTTACCCAGGCA 1521
Db 2936 TTACTCTGCTTTATTCACGAATGGTATGACGTCGCACTGCTCTGAAATGCC 2995
Qy 1522 ACTTTCTGGGGCTGGTACACCTCGATCTGGTCTGCTGCCAT 1563
Db 2996 ACATTTTGGATTATGTCGGCCAGCTTCTCTGGACTTGTGCT 3037

RESULT 6

AAV01536
ID AAV01536 standard; DNA; 3649 BP.
AC AAV01536;
XX
DT 08-JUN-1998 (first entry)
DE Human acylcoenzyme A:cholesterol acyltransferase (ACAT I) DNA.
XX
KW Acylcoenzyme A:cholesterol acyltransferase; ACAT I;
KW ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
KW inhibitor; atherosclerosis; hyperlipidaemia; human; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1397..3049
FT CDS /*tag= a
XX
PN WO9745439-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09460.
XX
PR 30-MAY-1996; 96US-0657620.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Sturley SL;
XX
DR WPI; 1998-032573/03.
DR P-PSDB; AAW43409.
XX
PT DNA encoding acylcoenzyme A: cholesterol acyltransferase II or
PT III - useful to identify inhibitors for treatment of
PT atherosclerosis or hyperlipidaemia
XX
PS Disclosure; Fig 5A 1-3; 121pp; English.
XX
CC This nucleic acid molecule encodes human acylcoenzyme A:cholesterol
CC acyltransferase (see AAW43409), or ACAT I. The invention relates to
CC isolated nucleic acids (see AAV01533-35) coding for human and mouse
CC acylcoenzyme A:cholesterol acyltransferase II and III (see
CC AAW43406-08), also designated ACAT related gene products (ARGP) 1
CC and 2. These can be used to identify inhibitors useful in the
CC treatment of atherosclerosis and hyperlipidaemia.
XX

SQ Sequence 3649 BP; 929 A; 749 C; 781 G; 1190 T; 0 other;
Query Match 25.7%; Score 404; DB 19; Length 3649;
Best Local Similarity 58.8%; Pred. No. 1.7e-90;
Matches 766; Conservative 0; Mismatches 510; Indels 26; Gaps 3;
Qy 287 CATCTCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTGATGG 346
Db 1737 CACCTCCAGAACAGAAAGATTTTATTCGAAGGCGCTCTCTCTTAGATGAACCTGTTG 1796
Qy 347 AGTTCAGCATTTCCGACCATCTACCATGTTTATCCCTGCTGCTGCTGCTGCTGCTGCTGCT 406
Db 1797 AGTGACCATCTACGACCAATATATACATTTTATGCGCTCTCTCTCTCTCTCTCTCTCT 1856
Qy 407 TCAGACCCCTGCGCATCTGACCTTCATGATGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 466
Db 1857 TCAGCACACTTCTAGTAGATTACATTTGATGAAGGAGGCTGCTGCTGCTGCTGCTGCTGCT 1916
Qy 467 TGATCTTACGCTTGGGACAGCTGCCATTTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 526
Db 1917 TGTCTTATGCTTTTGGCAAAATTTCTTACGCTTGTGTTGGACCTGGTGGATCATGTTCTCT 1976
Qy 527 CCACCTGTTGGCGCGTACCAGGCCCTACGCTGTGGCGGACGCTGAGCGCAGG 586
Db 1977 CTACATTTTTCAGTTCCTTCTTTCTGTTTCAACATTTGGCGCATGCTGCTATAGCAAGATT 2036
Qy 587 CGACGGGCTGGGCTGTGCGCTTTTAGCGCGCCACCGCTGGTGGTGGTGGTGGTGGTGGTGGT 646
Db 2037 CTCATCGCTGATCCGTTCTCTCTTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG 2096
Qy 647 TCC-----ACGTGGCGTGGAGCATCAGTCCCGCGCGCTCCCGTT 688
Db 2097 TTCTAGTTTGGACCAACATATGTTGTGTAGCATATACATGCCACAGCTTCCCGT 2156
Qy 689 GTGCTCTGCTTCGAGCAGGTTAGTTCCTGATGAAAAGTACTCTCTCTCTGAGAGG 748
Db 2157 TCATCATATATTCGAGCAGATTCGTTTGTATGAAGGCCCACTCATTTGTCAGAGAGA 2216
Qy 749 CTGTGCTGGGATCTTCTGCGCAGACGAGGTGAGGGATCCAGGCCCGCAGTTTCTCCA 808
Db 2217 ACCTGCTCGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTCTTCCAATACCTACA 2275
Qy 809 G-----CTACCTCTACTTCTCTTCTGCCCAACACTCATCTACAGGAGACTTACCCT 861
Db 2276 GTCAACCACTATTTGTACTTCTTATTTGCTCTTACCTTATCTACCGTGACAGCTATCC 2335
Qy 862 AGGACGCTCTATCTCAGGTGGAATTTATGCGCAAGAACTTTGCCAGGCGCTTGGGATGT 921
Db 2336 AGAATCCCACTGTAAGATGGGTTATGCTGCTATGAAGTTTGCACAGGCTTTTGGTTGC 2395
Qy 922 GTGCTCTATGCTCTCTCTCTGCGCGCTCTGTGTTCTCTCTTTCGCAACATGAGC 981
Db 2396 TTTTCTATGTGCTACTACATCTTTGAAAGCTTTGTGCGCCCTTGTTCGGAATATCAA 2455
Qy 982 CGAGAGCCCTTCAGACCGCTGCGCTGCTCTCTCTATCTGCTGCTGCTGCTGCTGCTGCTGCT 1041
Db 2456 CAGGAGCCCTTCAGCGCTGCTGCTCTCTCTCTATGTTTAACTCCATCTTTCGCCAGGT 2515
Qy 1042 ATCTTCTATGCT 1101
Db 2516 GTGCTGATCT 2575
Qy 1102 GAGATCTACGATTTGGAGACAGGATGTTCTTACCGGAGCTGGTGGAACTCAAGCTCTCTTC 1161
Db 2576 GAGATCTACGCTTTGGTACAGGATGTTCTTATAAGGATTTGGTGGAACTCCACGCTCATAC 2635
Qy 1162 TCCAACTACTACCGCACTTGGAGACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1221
Db 2636 TCCAACTATATAGAACCTTGGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2695
Qy 1222 CAGATGGCTGCGGCTCTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1281
Db 2696 AAGGACTTTCTCTGGTTTTTCTCCAAAGATTTCAAACTGCTGCTGCCATGTTAGCTGCTTT 2755

QY	1282	CTGGTCTCGGAGTGGCCCATGAGTATATCTTTCGTTTCGTCCTGGGGTTCCTCTATCCC	1341
Db	2756	GCTGTATCTGCTGTAGTACAGAAATATGCTTGGCTGTTCCTGACCTTTTCTATCCC	2815
QY	1342	GTTCATGCTGATACTCTTCCTTGTTCATTTGGAGGAATGTTGAACCTTCATGATGCATGACCAG	1401
Db	2816	GTGCTGTTTCGTCCTCTCATCTGTTTGGAAATGGCTTCAACTTCATTTGCAATGATAGT	2875
QY	1402	CGACCGCGCCGGCATGCAACGCTGCTGATGTGGACCATGCTGTTTCTAGCCAGGGAATC	1461
Db	2876	CGGAAAAAGCCGATTGGAAATGTTGTGATGTGGACTTCTCTTTTCTTGGCCATGGAGTC	2935
QY	1462	CAGGTCAGCCTGACTGCGCAGAGTGTATCGACGCGGCGCACTGCCCTTACCCAGGCA	1521
Db	2936	TTACTCTGCTTTTATTCACAGAATGGTATGCAGTCGGCACTGCTCTGCAAAAATCCC	2995
QY	1522	ACTTTCTGGGCGCTGGTGACACCTCGATCTTGGTCCCGCAT	1563
Db	2996	ACATTTTGGATTATGTCGGGCCAGTTCCTGGACTTGTCTGT	3037
RESULT 7			
AAT96368			
ID	AAT96368 standard; DNA; 3650 BP.		
XX	AAT96368;		
XX	21-MAY-1998 (first entry)		
DE	Human acyl-coenzyme A:cholesterol acyltransferase I DNA.		
XX	Acyl-coenzyme A: cholesterol acyltransferase I; ACAT; human;		
KW	sterol; esterification; arteriosclerosis; hyperlipidaemia;		
KW	antifungal; fungicide; ss.		
XX	XX		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	CDS	1397..3050	
FT		/tag a	
FT		/transl_except= (pos:2492..2495, aa:Val)	
FT		/note= "this codon has an apparent 1 nucleotide	
FT		insertion, which alters the reading	
FT		frame"	
XX	WO9745536-A1.		
XX	04-DEC-1997.	97WO-US09160.	
XX	30-MAY-1997;	96US-0657621.	
XX	30-MAY-1996;		
XX	(UYCO) UNIV COLUMBIA NEW YORK.		
PA	(INDV) UNIV INDIANA FOUND.		
XX	Bard M, Sturley SL, Yang H;		
PI	WPI: 1998-032644/03.		
DR	P-PSDB: AAW38416.		
XX	Yeast acyl:coenzyme A:cholesterol acyl:transferase related enzyme I		
PT	and II - useful to identify inhibitor for treatment of		
PT	hyperlipidaemia, arteriosclerosis and fungal invasion		
XX	Disclosure; Page 61-63; 111pp; English.		
PS			
XX	This DNA sequence includes a coding region for human macrophage		
CC	acyl-coenzyme A:cholesterol acyltransferase I (hACAT) (see AAW38416).		
CC	It has been used to search for homologous yeast genes (see AAW96369		
CC	and AAT96370) and subsequently to identify an additional human		
CC	isoform (see AAW38421). A novel claimed expression vector (1)		

comprises an isolated nucleic acid molecule encoding yeast wild type acyl-coenzyme A:cholesterol acyltransferase 1 (ARE1) (see AAM38417) or 2 (ARE2) (see AAM38418) operatively linked to a promoter. The vector and a claimed host-vector system can be used for the recombinant production of ARE1 or ARE2. The products can be used to identify novel ARE1 or ARE2 inhibitors. ARE2 inhibitors can be used to treat arteriosclerosis or hyperlipidaemia, as well-as to inhibit fungal growth or to treat fungal invasion (claimed).

Query Match	25.1%	Score 394.6	DB 19	Length 3650	
Best Local Similarity	58.9%	Pred. No. 3.7e-80			
Matches 767	Conservative	0	Mismatches 509	Indels 27	Gaps
QY	287	CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCTCTGTATGAGCTGATGG	346		
DB	1737	CACCTCCAGAACAGAAAGATTTTATTTGCAAGCGCTCTCTTAGATGAACATGCTTG	1796		
QY	347	AGGTGCAGCATTTCCGACACATCTACCAATGTTTCATCGCTGGCGCTGTGTGCTTTCATCA	406		
DB	1797	AAGTGGACCACATCAGAAACAATATATACATGTTTATTGGCCCTCCTCATCTCTTTATTC	1856		
QY	407	TCAGCACCCCTGGCCATCGACTTCATTGATGAGGCGAGCTGCTGCTGAGTTTGACCTAC	466		
DB	1857	TCAGCACACITGTAGTAGATTAACATTGATGAAGGAAGGCTGCTGCTGAGTTCAGCCTCC	1916		
QY	467	TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGGTGAACCTGGGTGCCCATGTTCTGT	526		
DB	1917	TGCTTATGCTTTTGGCAATTTCCCTACCGTTGTTTGGACCTGGTGGATCATGTTCTCTGT	1976		
QY	527	CCACCCCTGTTGGCGCGCTACCAAGGCCCTAGGCTGTGGCCAGGGCACCCTGGAGCGAGG	586		
DB	1977	CTACATTTTCAGTTTCCCTATTTTCTGTTTCAACATTTGGCGCACTGGCTATGCAAGAGTT	2036		
QY	587	CGACGGCGCTGGGCTGTGCGCTTTTAGCGCGCCACGCCCTGTGCTGTCCGCGTGC	646		
DB	2037	CTCATCCGCTGATCCGTTCTCTCTTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG	2096		
QY	647	TCC-----ACGTGGCGGTGGAGCATCAGCTCCCGCGGCGCTCCCGTT	688		
DB	2097	TTCTAGGTTTGGACCAACATATGTTGTGTAGCATATACATGGCCACACAGCTTCCCGGT	2156		
QY	689	GTGCTCGTCTTCGACGAGGTAGTTCCTGATGAAAGTACTCTCTTCCTGAGAGAGG	748		
DB	2157	TCATCATTTATTTTCGACGATTCGTTTGTGTAAGGCCCACTCATTTGTCAGAGAGA	2216		
QY	749	CTGTGCCCTGGGATCCTTCGTGCCAGAGAGGTGAGGGGATCCAGGCCCCAGTTTCTCCA	808		
DB	2217	ACGTGCCCTCGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTTTCCTCAATAGCTACA	2279		
QY	809	G-----CTACCTCTACTTCCCTCTTCGCCCAACACTCATCTACAGGAGACATTCACCT	861		
DB	2276	GTCAACCAAGTATTTGACTTTCTATTTCCTTCCCTACCCCTTATCTACCGTGACAGCTATCC	2335		
QY	862	AGGACGCCCTATGTCAGGTGGAATATGTGCCAAGAACTTTGCCAGGCCCTGGGATGT	921		
DB	2336	AGGAATCCCACTGTAAAGATGGGGTATGTGCTATGAAGTTCGACAGGCTTGTGGTGC	2399		
QY	922	GTGCTCTATGCTGCTTCATCCTCGGGCGGCTCTGTGTTCCCTGTCTTCCCAACATGAGC	981		
DB	2396	TTTTTCTATGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTGTTCGGAATATCAAA	2455		
QY	982	CGAGAGCCCTTCAGACCCCGTCCCTGGTGTCTCTA-TCCTGCATGCCACAGTTGCCAGG	1041		
DB	2456	CAGGAGCCCTTCAGCGCTCGTGTCTGTGCTCTATGTGGTATTTAACTCCATCTTGGCAGG	2511		
QY	1041	CATCTTCATGCTGTGCTCATCTCTTTTGGCCTTCCCTCATTTGCTGTGCTCAACGCCCTTTCG	1101		
DB	2516	TGTGCTGATCTCTCTCTTACTTTTTTTTGGCCCTTTTTCGACTGTGCTCAATGCCCTTTCG	2571		
QY	1101	CGAGATGCTACGATTTGGAGACAGATGTTCTACCGGGACTGGTGGAACTCAACGCTCTT	1161		

CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1885 BP; 410 A; 514 C; 504 G; 457 T; 0 other;
 Query Match 11.0%; Score 172; DB 23; Length 1885;
 Best Local Similarity 51.9%; Pred. No. 8.5e-33;
 Matches 413; Conservative 0; Mismatches 380; Indels 3; Gaps 1;
 QY 774 ACAGAGTGGAGGATCCAGGCCCGGAGTTTCTCCAGTACCTCTACTCTCTCTCTGCCC 833
 DB 1001 AGGCAGTGCAGCGACCTTTTGGCCGCGCTGAGCTGTACACGCTACTTTTGTTCGACC 1060
 QY 834 AACACTCATCTACAGGAGACTTACCTAGGACGCCCTATGTCCAGTGGGAATATGTGGC 893
 DB 1061 CACGCTTATCTACGAGACAGCTACCCGCGACCTCCACATCGCTGGAAGTTGGCCT 1120
 QY 894 CAAGAACTTTGCCAGGCCCTGGGATGTGCTCTATGCTGTCTTCACTGCGGCCGCT 953
 DB 1121 GAATCGACTGTGGAGTGGTGGCCATAGCTTCTGTACGCGTTCATCCATGAGCGCA 1180
 QY 954 CTGTGTTCTGCTTTGCCAACATGACCGAGAGCCCTTCAGACCCGCTGCCCTGTGCT 1013
 DB 1181 CATCCAGGACACTTCCGACAGTACGACTGGAACCAATGGGACCTCCGAGCTGATCCT 1240
 QY 1014 CTCTATCTGATCCACGCTTCCAGGACATCTTCATGCTGTCTCATCTCTCTTTGCTT 1073
 DB 1241 CAAGCTGTGGCATGTGCTGCCAGCGGGTATCTTTCTGTGGGCTCTACCTAAT 1300
 QY 1074 CCTCATCTGTGCTCAACGCTTTTGGCGAGTGTACGATTTGGAGACAGGATGTCTA 1133
 DB 1301 CCTGACTCGTGGTGAATTCACGTGGAGCTCTACGCTTCGGTGTATGATGAATGTCTA 1360
 QY 1134 CCGGACTGTGGAACTCAAGCTCTTCTCAACTACTACGCACTTGGAACTGGTGT 1193
 DB 1361 CAAGGACTGGTGGAGCTGCGACACTTACGATGGCTACTACAACTTGGATGTCTGCT 1420
 QY 1194 CCATGACTGGCTTACAGCTACGTATGATGAGTGGCTGCGGCTCCCTTGGTGGCCGCGC 1253
 DB 1421 GCAGGACTGGCTGACGAGTACGTTACAGGATATGTACACTCATGTGTTCCGAGGTT 1480
 QY 1254 CGAGGGGTACCATGCTGGTGTGTTCTTCTCCGCTGCTCCGCTGCTGCTGATATCTT 1313
 DB 1481 CAAGTGGCCGCTGCTGGGAGTGTTCATGATCTCCGCTGCTGCTGCTGCTGCTGCT 1540
 QY 1314 CTGCTTCTGCTGGGTTCTTCTATCCGCTCATGCTGATCTCTCTCTCTCTCTCTCT 1373
 DB 1541 CGGCTTTGCCCTGCAATGTCTTCTCCAGTGTGTTCTTCTTCTTGGGCTGCTGGTGT 1600
 QY 1374 AATGTTGAATTCATGATGATGACAGCCAGCCGCGCCGCGATGGAACGTTGCTGATGTG 1433
 DB 1601 TGCCTTGGTATCTTAATGCGAGTGTCTCAAAAGTATG--GCAACATCTTCTCTGTG 1657
 QY 1434 GACCATGCTGTTTACGCGAGGAAATCCAGGTGACGCTGCTACTGCTCCAGGAGTGTGACG 1493
 DB 1658 GTTCTCTGATCTCTGGGAAATGCGACGCTGATCTCACTATACGCAATGAGCATACGC 1717
 QY 1494 ACGGCGGCACTGCCCTTACCCAGGCAACTTTCTGGGGGTGGTGTACACCTCGATCTTG 1553
 DB 1718 CTAAGAAGACTGCAACCTAAGCAACGAGATGTGACGATCGCTGCTGCTGCGCGGTATG 1777
 QY 1554 GTCTTGGCATCTAG 1569
 DB 1778 GCGCTGCTACAAATTAG 1793

RESULT 10
 ID ABL15694
 XX ABL15694 standard; cDNA; 2657 BP.
 AC ABL15694;

XX 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41564.
 DE
 XX Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 KW Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI: 2001-656860/75.
 DR P-PSDB; ABB71591.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 41564; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2657 BP; 704 A; 610 C; 624 G; 719 T; 0 other;
 Query Match 11.0%; Score 172; DB 23; Length 2657;
 Best Local Similarity 51.9%; Pred. No. 9.6e-33;
 Matches 413; Conservative 0; Mismatches 380; Indels 3; Gaps 1;
 QY 774 ACAGAGTGGAGGATCCAGGCCCGGAGTTTCTCCAGTACCTCTACTCTCTCTCTGCCC 833
 DB 185 AGGCAGTGCAGCGACCTTTTGGCCGCGCTGAGCTGTACACGCTACTTTTGTTCGACC 244
 QY 834 AACACTCATCTACAGGAGACTTACCTAGGAGGCCCTATGTCCAGTGGGAATATGTGGC 893
 DB 245 CACGCTTATCTACGAGACAGTACCCGCGACCTCCACATCGCTGGAAGTTGGCCT 304
 QY 894 CAAGAACTTTGCCAGGCCCTGGGATGTGCTCTATGCTGCTCTCTCTCTGCGGCCCT 953
 DB 305 GAATCGACTGTGGAGTGGTGGCCATAGGCTTCTCTAGCGGTTTCATCCATGAGCGCA 364
 QY 954 CTGTGTTCTCTCTTCCAACTAGCGGAGGCCCTTCAGACCCGCTGCCCTGTGCT 1013
 DB 365 CATCCAGGACACTTCGGACAGTACGAGTGGAACTGGGACCTCCAGCTGATCCT 424
 QY 1014 CTCTATCTGATGCCAGCTTGGCCAGCATCTTTCATGCTGCTGCTCACTCTTTGCTT 1073
 DB 425 CAAGCTGTTCGGCATGATGCTGCCAGCGGCTGATCTTCTGTGCGGCTCTACCTAAT 484
 QY 1074 CCTCCATGCTGGCTCAACGCCCTTGGCCGAGATGCTAGGATTTGGAGACAGGATGTCTA 1133
 DB 485 CCTGCACCTGCTGGTGAACCTTACGTCGGAGCTGCTACGCTTCGGTGTGATGAATGTCTA 544

RESULT 12

AAQ63210

ID AAQ63210 standard; cDNA; 996 BP.

XX AC AAQ63210;

XX 03-JAN-1995 (first entry)

XX Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).

XX Acetyl coenzyme A: cholesterol acetyltransferase; ACAT; disease;

XX diagnosis; detection; screening; treatment; prophylaxis;

XX hypercholesterolaemia; atherosclerosis; antisense; probe;

XX identification; ss.

XX Homo sapiens.

XX WO9409126-A.

XX 28-APR-1994.

XX 12-OCT-1993; 93WO-US09704.

XX 14-OCT-1992; 92US-0959950.

XX 10-SEP-1993; 93US-0121057.

XX (DART-) DARTMOUTH COLLEGE.

XX Chang CCY, Chang T;

XX WPI; 1994-151312/18.

XX Acetyl coenzyme A: cholesterol acetyl-transferase and nucleic

XX acid sequence encoding it - used to correct enzyme deficiencies

XX and screen for enzyme inhibitors

XX Claim 13; Figure 3; 52pp; English.

XX The acetyl coenzyme A: cholesterol acetyl-transferase (ACAT) gene

XX sequence enables the screening of human populations for abnormal

XX human ACAT activities for disease diagnosis. It provides

XX information concerning the catalytic mechanism of ACAT and allows

XX the design of drugs serving as specific ACAT inhibitors, desirable

XX for the prevention and/or treatment of human hypercholesterolaemia

XX and human atherosclerosis. It also allows the design of antisense

XX DNAs or RNAs to inhibit ACAT production, or probes to identify

XX different forms of human ACAT or ACAT from different animal species.

XX This sequence is a human ACAT cDNA clone designated Cl.

XX Sequence 996 BP; 258 A; 219 C; 207 G; 312 T; 0 other;

XX Query Match 8.6%; Score 134.6; DB 15; Length 996;

XX Best Local Similarity 53.1%; Pred. No. 1.4e-23;

XX Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGACGCTCCTCTGATGAGTGATGG 346

DB 262 CACCTCCAGAAACAGAAAGATTATTTAATGCAAGGCGCTCTCTTAGATGAACGTGTG 321

QY 347 AGGTGCAGCATTTCCGACCATCTACCATGTTTCATCGCTGGCTGTGTCTTTCATCA 406

DB 322 AAGTGACCATCATGACATATATACATGTTTATTTGCTCCCTCCTCATTCTTTATCC 381

QY 407 TCAGCACCTGGCCATCGACCTCATATGATGAGGCGCTGCTGCTGG--AGTTTGACCT 464

DB 382 TCAGCACACTTGTAGTAGATTACATGATGATGAAGGAGGCTGGTGTGCAAGTTACGCT 441

QY 465 ACTG-ATCTTCAGCTTCGACGAGCTGACATGGCGCTGGTACCTGGTGGCCATGTTTC 523

DB 442 CCGTCTTATGCAATTTGGCAAAATTTCTACCGTTGTTGGACCTGGTGGATCATGTTCC 501

QY 524 TGTCCACCTGTTGGCGCGGTACACAGGCGCTACGCGCTGGCGGAGGCGACCTGGACGC 583

Db 502 TGTCTACATTTTCAGTTCCTATTTTCTGTTTCAACATTGGCGCACTGGCTATACAGA 561

QY 584 AGGCGACGGGCTGGGCTGTGGCTTTTATAGCGCCCGCCAGCGCTGGTGCTC----- 633

Db 562 GTTCTCATCCGCTGATCGGTTCTCTCTTCCATGGCTTTCTTTTTCATGATCTTCCAGATTG 621

QY 634 ----TGGCGCCTCCGCTGTCACGTCGCGGTGGAGCATCAGCTCCCGCGGCTCCCGTTGT 590

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QY 691 GTCCCTGGCTTCGACGAGCTAGGTTCCCTGATGAAAAGCTACTCTCTCTCTGAGAGGCT 750

Db 682 TTATCATTTATTCGACGAGATCGTTTGTATGAAGGCCCACTCATTTGTCTAGAGAGAC 741

QY 751 GTCCCTGGGATCCTTCGTCGACGAGGTGAGGGATCCAGGCC-----CCAGTTTCT 805

Db 742 GTCCCTCGGTACTAATTCAGCTAAGGAGAAATCAAGCACTGTTCATATACCTACAGTCA 801

QY 806 CGAGCTACCTCTACTTCTCTCTGTCGCCCAACTCATCTACAGGGAGACTTACCCTAGGA 865

Db 802 ACCAGTATTGTTACTTCTTATTGCTCTCTACCTTATCTACCGTGACAGCTATCCAGGA 861

QY 866 CGCCCTATGTCAGGTGGAATTTATGTCGCAAGAACTTTGCCAGGCGCTGGGATGTGTGC 925

Db 862 ATCCCACTGTAGATGGGTTATGTTGCTATGAAGTTTCACAGGCTCTTTGGTTGCTTT 921

QY 926 TCTATCCCTGCTTCATCTCTGGGCGGCTCTGTGTTCTCTGTTTGGCAACATGAGCCGAG 985

Db 922 TCTATGCTACTACATCTTTTGAAGGCTTTGTGCCCGCTTTGTCGGAATATCAACAGG 981

QY 986 AGCCCTTCAGCACCC 1000

Db 982 AGCCCTTCAGCGCTC 996

RESULT 13

AAV01539

ID AAV01539 standard; cDNA; 983 BP.

XX AC AAV01539;

XX 08-JUN-1998 (first entry)

XX Human acylcoenzyme A:cholesterol acyltransferase II (ACAT II) DNA.

XX Acylcoenzyme A:cholesterol acyltransferase; ACAT I;

XX ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;

XX inhibitor; atherosclerosis; hyperlipidaemia; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..660

XX /*tag= a

PN WO9745439-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US09460.

XX 30-MAY-1996; 96US-0657620.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Sturley SL;

XX WPI; 1998-032573/03.

XX P-PSDB; AAW43412.

XX DNA encoding acylcoenzyme A: cholesterol acyltransferase II or

XX III - useful to identify inhibitors for treatment of

XX atherosclerosis or hyperlipidaemia


```
XX This isolated nucleic acid molecule encodes human acylcoenzyme
CC A:cholesterol acyltransferase II (see AAW43406), or ACAT related gene
CC product 1 (ARGP-1), that is expressed at high levels in intestine
CC and is a candidate for sterol esterification in these tissues. It
CC was identified following database searching for human ACAT-related
CC sequences and use of PCR and RACE to obtain full-length sequences.
CC An isolated nucleic acid (see AAV01534) for human ARGP-2 (see AAW43407)
CC was also identified. Also claimed are host vector systems for
CC production of ARGP polypeptides, and transgenic non-human mammals.
CC ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a
CC subject who has an imbalance in sterol levels due to a defect in
CC sterol esterification. A claimed oligonucleotide capable of
CC specifically hybridising to a unique sequence of nucleotides in the
CC isolated nucleic acid molecule, or a vector expressing the
CC oligonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2.
CC The wild-type enzymes can be used to identify an inhibitor, useful
CC in the treatment of atherosclerosis or hyperlipidaemia.
XX
SQ Sequence 1521 BP; 277 A; 489 C; 412 G; 343 T; 0 other;

Query Match 6.1%; Score 95; DB 19; Length 1521;
Best Local Similarity 58.7%; Pred No. 1.2e-13;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGCATGCCACGTTGCCAGGATCTTCATGCTGCTCATCTCTTTTGCTTCCCTCC 1078
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1079 ATTGCTGGCTCAACGCTTTGCCGAGATGCTAGGATTTGGAGACAGGATGTTTACCGGG 1138
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 785 ACTCTGCTGCTGAATGCCGCTGGCTGAGCTCATGTCAGTTGGAGACCGGGAGTTCTACCGGG 844
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1139 ACTGTGGAACTCAAGCTCTTCTCCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 845 ACTGTGGAACTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACTCCCTGTGCACA 904
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1199 ACTGGCTGTACAGCTACGTTATCAGGATGGGCTCGGCTCCTTGGTCCCGGGCCGAG 1258
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 905 AGTGGTGCAATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCAGCAGCAAGT 958
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1259 GGGTAGCCATGCTGGGTGTGTTCTCGGCTCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 959 GGATGCCAGGACAGGGGTGTTCTTGGCTCGGCTTCTTCCACGAGTACCTGGTGAGCG 1018
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1319 TCGTCTCTGGGTCTTTC 1335
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1019 TCCCTCTGCGAATGTTTC 1035
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Search completed: April 30, 2003, 13:20:03
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:13:06 ; Search time 53 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1564.2	99.7	2040	3	US-09-165-042-4
2	405.6	25.9	4011	1	US-08-121-057-3
3	405.6	25.9	4011	2	US-08-509-187D-3
4	405.6	25.9	4011	2	US-09-121-396-3
5	405.6	25.9	4011	5	PCT-US93-09704A-3
6	359.8	22.9	4079	1	US-08-121-057-2
7	359.8	22.9	4079	2	US-08-509-187D-2
8	359.8	22.9	4079	2	US-09-121-396-2
9	359.8	22.9	4079	5	PCT-US93-09704A-2
10	134.6	8.6	996	1	US-08-121-057-1
11	134.6	8.6	996	2	US-08-509-187D-1
12	134.6	8.6	996	2	US-09-121-396-1
13	134.6	8.6	996	5	PCT-US93-09704A-1
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15	95	6.1	1976	3	US-09-165-042-2
16	81.4	5.2	1650	4	US-09-103-754A-2
17	79.8	5.1	1766	4	US-09-326-203A-15
18	79.8	5.1	1766	4	US-09-326-203A-16
19	56.8	3.6	7218	1	US-08-232-463-14
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23	42	2.7	3358	1	US-09-553-736-2
c 24	41.2	2.6	7218	1	US-08-232-463-14
25	40	2.5	629	4	US-09-103-754A-3
26	39.8	2.5	2970	4	US-09-110-517-3
c 27	39.8	2.5	5173	1	US-08-242-677-1

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28 39.4 2.5 20235 1 US-07-642-734C-3
29 39.4 2.5 20235 3 US-08-439-009A-3
30 39.2 2.5 1469 5 PCT-US92-08258-1
c 31 39.2 2.5 2353 5 PCT-US92-06840-1
32 39 2.5 289 4 US-09-007-005-17
33 39 2.5 289 4 US-09-244-796-17
34 39 2.5 2474 2 US-08-666-392A-2
35 39 2.5 2474 4 US-09-199-926-2
36 39 2.5 33529 4 US-09-144-085-3
c 37 38.8 2.5 30001 1 US-08-125-468-1
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39 38.6 2.5 2080 2 US-08-878-563A-2
40 38.6 2.5 2080 4 US-09-270-117-2
41 38.6 2.5 2430 4 US-09-105-537-23
42 38.6 2.5 13613 4 US-09-105-537-3
c 43 38.4 2.4 500 3 US-09-141-000-2
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c 45 38.4 2.4 696 4 US-09-461-697-191

ALIGNMENTS

RESULT 1
US-09-165-042-4
; Sequence 4, Application US/09165042
; Patent No. 6100077
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165,042
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Yeast
US-09-165-042-4

Query Match 99.7%; Score 1564.2; DB 3; Length 2040;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGAGCCAGGCGGGCGCGTCTGCGTTCGAGAGGACAGAGGGCTGGAGGGGAGCGG 60
Db 52 ATGGAGCCAGGCGGGCGCGTCTGCGTTCGAGAGGACAGAGGGCTGGAGGGGAGCGG 111
QY 61 GAGCGCCACCTGTGGAGATGGAACACTGAGAGCGACAGAGCCCGGACTTGGTACAA 120
Db 112 GAGCGCCACCTGTGGAGATGGAACACTGAGAGCGACAGAGCCCGGACTTGGTACAA 171
QY 121 TGGACCCGACACATGAGGCTGTGAAGGCACAAATTCCTGGAGCAAGCGGAGGACAACTG 180
Db 172 TGGACCCGACACATGAGGCTGTGAAGGCACAAATTCCTGGAGCAAGCGGAGGACAACTG 231
QY 181 AGGAGCTCTGATGTCGGGCGCATGCGGAGGCTATACAACTTACCCATCACAAGACAA 240
Db 232 AGGAGCTCTGATGTCGGGCGCATGCGGAGGCTATACAACTTACCCATCACAAGACAA 291
QY 241 CCTCTGCCCGCCACCTCCCGGCTTCTTGGAGCAGCAGGAGCCCGGAGGAGGAGGAGG 300
Db 292 CCTCTGCCCGCCACCTCCCGGCTTCTTGGAGCAGCAGGAGCCCGGAGGAGGAGGAGG 351
QY 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTAGTGTGATGAGTGTGAGGAGTTC 360
Db 352 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTAGTGTGATGAGTGTGAGGAGTTC 411
QY 361 CGCACCATCTACACATGTTTCATCGTGCCTGCTGTGTCTTCATCATCAGCACCCCTGGCC 420

Db 412 CGCACCATTACACATGTTTCATCGCTGGCTGTGTGTCTTCATCATCAGCACCTGGCC 471
Qy 421 ATGACTTATTCATGAGGCGAGGCTGTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480
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Qy 721 ATGAAAAGCTACTCTTCCTGAGAGAGCTGTGCTGGGATCTCTGTCGACAGCGAGT 780
Db 772 ATGAAAAGCTACTCTTCCTGAGAGAGCTGTGCTGGGATCTCTGTCGACAGCGAGT 831
Qy 781 GAGGGATCCAGGCGCGGCTTCTCCAGCTACTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
Db 832 GAGGGATCCAGGCGCGGCTTCTCCAGCTACTCTTCTTCTTCTTCTTCTTCTTCTTCT 891
Qy 841 ATCTACAGGAGACTTACCTTAGGACCCCTATGTCAGGTGGATATGTGGCGCAAGAC 900
Db 892 ATCTACAGGAGACTTACCTTAGGACCCCTATGTCAGGTGGATATGTGGCGCAAGAC 951
Qy 901 TTTGCCAGGCGCTGGATGTGCTGTATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 960
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Qy 1561 CATACCTAG 1569
Db 1612 CATACCTAG 1620

RESULT 2
US-08-121-057-3
; Sequence 3, Application US/08121057
; Patent No. 5484727
; GENERAL INFORMATION:
; APPLICANT: CHANG, TA-YUAN
; APPLICANT: CHANG, CATHERINE C. Y.
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: BOSTON
; STREET: 60 STATE STREET, SUITE 510
; STATE: MA USA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,057
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: LAMPORT HAMMITTE, ANN.
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-2700
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1397..3046
; US-08-121-057-3

Query Match 25.9%; Score 405.6; DB 1; Length 4011;
Best Local Similarity 58.9%; Pred. No. 1.1e-94;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

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Db 1797 AAGTGGACCATCATAGAACATATATCATGTTTATGGCCCTCCTCATCTCTTTATCC 1856
Qy 407 TCAGCACCCTGGCCATCGACTTCATTTGATGAGGCGAGGCTGCTGCTGAGTTGACCTAC 466
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Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATGGCGCTGGTGGTACCTGGGTGCCCATGTTTCTGT 526

Db 1917 TGTCTTATGCTTTTGGCAAAATTCCTACCGTTGTTTGGACCTGGTGATCATGTTCCCTGT 1976
QY 527 CCACCCGTGTGGCGGTACAGGCCCTACGGCTGTGGCCAGGGGCACCTGGACCGAGG 586
Db 1977 CTACATTTTCAGTTCCTTATTTTCTGTTTCAACATTTGGCGCACTGCTGTATAGCAAGATT 2036
QY 587 CGACGGCCCTGGCGTGTGGCGTTTATAGCCGCCACACGCCCTGTGTCTCGCGGCTCCCGG 646
Db 2037 CTATCCGCTGATCCGTTCTCTCTCCATGCGTTCTTTTCATGATCTTCCAGATTGGAG 2096
QY 647 TCC-----ACGTGGCGGTGGAGCATCAGCTCCCGCGCGGCTCCCGTT 688
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Db 2876 CGGAAAAGCCGATTTGGAATGTTCTGATGTGGACTTCTCTTTCTTTGGAATGAGTC 2935
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QY 1522 ACTTTCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563
Db 2996 ACATTTTGGATATGCTGGGCCACGCTTCTGACTTGTGCT 3037

RESULT 3
US-08-509-187D-3
; Sequence 3, Application US/08509187D
; Patent No. 5834283
; GENERAL INFORMATION:
; APPLICANT: Chang, Te-Yuan and Chang, Catherine C.Y.
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/509,187D
; FILING DATE: 31-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lamport Hammitte, Ann
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033cpdv
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1397..3046
; US-08-509-187D-3

Query Match 25.9%; Score 405.6; DB 2; Length 4011;
Best Local Similarity 58.9%; Pred. No. 1.1e-94;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;
QY 287 CATCCCTCGGGAAACAGAAAGTTTTCATCATCGCAAGTCCCTGCTGTGATGAGCTGATGG 346
Db 1737 CACCTCCAAACAGGAAGATTTTATTCGAAGGCGCTCTCTCTTAGATGAAGCTGCTTG 1796
QY 347 AGGTGAGCATTTCCGACCATCTACCATGTTTCATCGCTGGCCTGTGTGTTCTTCATCA 406
Db 1797 AAGTGACCAACATCAGAACAAATATACATGTTTATTCGCCCTCCTCATCTCTTTATCC 1856
QY 407 TCAGGACCCCTGGCCATCGACTTCATGATGAGGCGAGGCTGCTGGAGTTTGACCTAC 466
Db 1857 TCAGCACACTTGTAGTAGATTACATTCATGTAAGGAAGGCTGTGCTGTTAGTTTCAGCTCC 1916
QY 467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
Db 1917 TGTCTTATGCTTTTGGCAAAATTTCTTACCGCTTGTGGACCTGCTGGATCATGTTCTCTGT 1976
QY 527 CCACCCCTGTTGGCGGCTACAGGCCCTACGGCTGTGGGCCAGGGCACCTGGACCGAGG 586
Db 1977 CTACATTTTCAGTTCCTTATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAGATT 2036
QY 587 CGACGGGCTGGGCTGTGCGCTTTTAGCCGCCACACCGCTGTGCTCTGCGCGCTCCCGG 646

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Db 2037 CTCATCGCTGATCCGTTCTCTCTTCATGCTTCTTTTCATGATCTTCACAGATTGGAG 2096
Qy 647 TCC-----ACGTGCGCTGGAGATCAGCTCCCGCGCCGCTCCCGTT 688
Db 2097 TTTAGTTTGGACCAACATATGTTGTAGCATATACATGCCACAGCTTCCCGGT 2156
Qy 689 GTGTCCTGGTCTTCGACGAGTTAGTTCTGTATGAAAGCTACTCTCTTCTGAGAGAGG 748
Db 2157 TCATCATATATTCGACGAGATTCGTTTGTATGAAAGGCCACTCATTTGTTCAGAGAGA 2216
Qy 749 CTGTGCTTGGATCTTCGTCGCCAGAGGTGAGGGATCCAGGCCGCCAGTTTCTCCA 808
Db 2217 ACGTGCGCTCGGGTACTAAAT-TCAGTAAAGAGAAATCAAGCACTGTTCCTCAATACCTACA 2275
Qy 809 G-----CTACCTCTACTTCTCTCTGCCCCAACACTCATCTACAGGAGACTACCCCT 861
Db 2276 GTCAACCAATTTGTACTCTTATTTGCTCCCTACCTTATACCGTGACAGCTATCCC 2335
Qy 862 AGGACGCCCTATGTCAGGTGGAATATATGAGCCAAAGAACTTTGCCAGGCCCTGGGATGT 921
Db 2336 AGGAATCCACTGTAAAGATGGGTTATGTCGCTATGAATTTGCACAGGCTTTGGTTGC 2395
Qy 922 GTGCTCTATGCTGCTCTCACTCTGCGCGCTCTGCTGCTCTGCTTTCGCAATCAGC 981
Db 2396 TTTTCTATGTACTACTACTTTTGAAGGCTTTGCGCCCTTGTTCGGAATATCAA 2455
Qy 982 CGAGAGCCCTTCAGCACCGCTGCTGCTCTCTATCTCTGATGCGAGTTTGCCAGGC 1041
Db 2456 CAGGAGCCCTTCAGCGCTGCTGCTGCTGCTATGTTTAACTCCATCTTCCAGGT 2515
Qy 1042 ATCTTCTGCTGCTGCTCATCTCTTTGCCCTTCTCTCACTGCTGCTCAAGCCCTTTGCC 1101
Db 2516 GTGCTGATCTCTCTCTACTTTTGTGCTTTTGGCTTTTGGCACTGCTGCTCAATGCTTGT 2575
Qy 1102 GAGATGCTACGATTTGGACAGGATGTTTACCGGGCTGCTGCTGCTGCTCAACTCACTTC 1161
Db 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTAAGGATTTGGTGAACCTCCAGCTATAC 2635
Qy 1162 TCCAACTACTACCGCACTTGGAACTGTTGCTGCTCTCTATCTCTGATGCGAGTTTGCCAGGC 1221
Db 2636 TCCAACTATATAGAACCTGGAATGTTGCTGCTGCTGCTGCTATATCTATGCTTAC 2695
Qy 1222 CAGGATGGCTGCGCTCTCTTGGTCCCGCGCGCGAGGGTGAACCTGCTGGTGTGTTTC 1281
Db 2696 AAGGACTTTCTCTGTTTTTCTCCAAAGATTCAAATCTGCTGCACTGCTGCTGCTT 2755
Qy 1282 CTGGTCTCGGAGTGGCCCATGAGTATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341
Db 2756 GCTGATCTGCTGATGACAGCAATATGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815
Qy 1342 GTCATGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
Db 2816 GTGCTGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2875
Qy 1402 CCGACCGCGCGCGCTGGAACCTGCTGATGCTGACCATGCTGCTTCTAGGCGAGGAAATC 1461
Db 2876 CGGAAAACCGGATTTGGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2935
Qy 1462 CAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
Db 2936 TTAATCTGCTTTTATCTCAAGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2995
Qy 1522 ACTTTCTGGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563
Db 2996 ACATTTTGGATTTATGCTCGGCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3037

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RESULT 4

US-09-121-396-3
; Sequence 3, Application US/09121396
; Patent No. 5968749
; GENERAL INFORMATION:

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; APPLICANT: CHANG, TA-YUAN
; APPLICANT: CHANG, CATHERINE C. Y.
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,396
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/509,187
; FILING DATE: 07/31/95
; ATTORNEY/AGENT INFORMATION:
; NAME: LAMPORT HAMMITTE, ANN.
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-2700
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-121-396-3

```

Query Match 25.9%; Score 405.6; DB 2; Length 4011;

Best Local Similarity 58.9%; Pred. No. 1,1e-94; Indels 26; Gaps 3;
Matches 767; Conservative 0; Mismatches 509;

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Qy 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTGAGG 346
Db 1737 CACCTCCAGAACAGAAAGATTTTATGCAAGGCGCTCTCTTAGATGAAGTCTGTG 1796
Qy 347 AGGTGACAGATTTCCGCAACCATCTACCACATGTTTCATCGCTGGCCTGTGTCTTCATCA 406
Db 1797 AAGTGGACCAATCAGAACAAATATATCATGTTTATGCGCCCTCCTCATCTCTTTATCC 1856
Qy 407 TCAGCACCTGGCCATCGACTTCATTTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTAC 466
Db 1857 TCAGCACATTTGTAGTATGATTTGATGAGGAGGCTGCTGCTGAGTTTACGCTCC 1916
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGCGCTGGTGGTACCTGCGGCTCCCATGTTCTGT 526
Db 1917 TGTCTATGCTTTTGGCAAAATTTCTACCGCTGTTTGGACCTGCTGATCATGTTCTCTGT 1976
Qy 527 CCACCTGTTGGCGCGTACCAGCCCTACGGCTGTGGCCAGGGGCGACCTGGAGCAGG 586
Db 1977 CTACATTTTCAAGTTTCCCTATTTTCTGTTTCAACATTTGGCGCACTGGGCTATAGCAAGAGTT 2036
Qy 587 CGACGGGCTGGGCTGCTGCTGCTTTTAGCGCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
Db 2037 CTCATCCCTGATCCGTTCTCTCTTCCATGCTTCTTTTCATGATCTCTCCAGATTGGAG 2096
Qy 647 TCC-----ACGTGCGCGCTGGAGCAATCAGCTCCCGCGCCGCTCCCGTT 688
Db 2097 TTCTAGGTTTGGACCAACATATGTTGTTAGCATATACACATGCGCCAGCTTCCCGGT 2156
Qy 689 GTGCTCTGCTCTTCAGCAGGTTAGTTTCTTCATGATGATGATGATGATGATGATGATGATGAT 748

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Db 2157 TCATCATTTATATTCAGCAGATTCGTTTTGTATGAAGGCCCACTCATTTGTCAGAGAGA 2216
Qy 749 CTGTGCTGGGATCCTTCGTCAGACGAGGTGAGGGATCCAGGCCCGCTTCTCCA 808
Db 2217 ACGTGCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAACTACATA 2275
Qy 809 G-----CTACCTCTACTTCTCTCCCAACACTCATCTACAGGAGACTTTACCT 861
Db 2276 GTCAACACGATATTGTACTTCTTATTTGCTCCTACCTTATACCGGTGACAGCTATCCC 2335
Qy 862 AGGAGGCCCTATGTCAGGTGAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGT 921.
Db 2336 AGGAATCCCACTGAAGATGGGTATGTCGTATGAAGTTTGCACAGCTTTGGTGTGC 2395
Qy 922 GTGCTCTATGCTGCTTCATCTCGGCCGCTCTGTCTGTCTGTTCCCAACATGAGC 981
Db 2396 TTTTCTATGATGCTACTACATCTTTGAAGGCTTTGTGCCCTTGTTCGGAATATCAA 2455
Qy 982 CGAGAGCCCTTCAGACCCGCTGCCCTGTGTCTCTATCTTCATGCAAGCTTGCAGGC 1041
Db 2456 CAGGAGCCCTTCAGCGCTCGTGTCTGTCTCTATGATGATTAACATCCATCTTGCCAGT 2515
Qy 1042 ATCTTCATGCTGCTCATCTTTTGCCTTCTCTCCATTTGCTGGCTCAAGCCCTTTGCC 1101
Db 2516 GTGCTGATCTCTCTCTTACTTTTGTGCTTGTGCTGCTGCTCAATGCCCTTTGCT 2575
Qy 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAGTGTGAAGCTCAACGTCCTTC 1161
Db 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAGGATTTGGTGAACCTCCACGTCATC 2635
Qy 1162 TCCAACTACTACGCACTTTGGAACGTTGGTGCTGATGCTGCTGATGCTGATGCTGAT 1221
Db 2636 TCCAACTATTATAGAACTGGAATGTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2695
Qy 1222 CAGGATGGCTGCGGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281
Db 2696 AAGGATTTCTGCTGCTTCTTCCAAAGATTTCAAACTGCTGCTGCTGCTGCTGCTGCTGCT 2755
Qy 1282 CTGTGCTCGGAGTGGCCATGAGTATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341
Db 2756 GCTGTATCTGCTGATGACAGAAATATGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815
Qy 1342 GTCATGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
Db 2816 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2875
Qy 1402 CGCAGCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461
Db 2876 CGGAAAAGCCGATTTGGAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2935
Qy 1462 CAGGTGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
Db 2936 TTACTCTGCTTATTTCTCAAGATGGTATGACGCTCGGCACTGCTGCTGCTGCTGCTGCTGCTGCT 2995
Qy 1522 ACTTTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563
Db 2996 ACATTTTGGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3037
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RESULT 5.

PCT-US93-09704A-3

; Sequence 3, Application PC/TUS9309704A

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 9

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09704A
; FILING DATE: October 12, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. SER. NO. 959,950
; FILING DATE: October 14, 1992
; APPLICATION NUMBER: U.S. SER. NO. 121,057
; FILING DATE: September 10, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAMPORT HAMMITTE, ANN.
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033CP
; TELEPHONE: (617) 227-2700
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US93-09704A-3
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Query Match 25.9%; Score 405.6; DB 5; Length 4011;
Best Local Similarity 58.9%; Pred. No. 1.1e-94;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

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Qy 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTATGATGAGCTGATGG 346
Db 1737 CACCTCCAGAAAGAAAGATTTTATTTGCAAGCGCTCTCTCTTAGATGAACGTCTG 1796
Qy 347 AGGTGCACGATTTCCGACCATCTACACATGTTTTCATCGCTGGCCCTGTGTCTTTCATCA 406
Db 1797 AAGTGGACCATCAGAACATATATACATGTTTATTTGCCCTCTCATCTCTCTTATCC 1856
Qy 407 TCAGCACCTTGGCCATCGACATTTGATGATGAGGGCAGGCTGCTGCTGGAGTTTGACCTAC 466
Db 1857 TCAGCACACTTGTAGTAGATTACATTTGATGAAGGAAGCTGGTGTGATGATGATGATGAT 1916
Qy 467 TCATCTTACGCTTCGGACAGCTGCCATTTGGCCCTGCTGACCTGGTGGTGGTGGTGGTGGT 526
Db 1917 TGTCTATGCTTTTGGCAAAATTTCTACCGTTGTTGGACCTGGTGGATCATGTGCTCTGT 1976
Qy 527 CCACCTCTTGGCGCGCTACCAAGCCCTACGCGCTGTGGGCCAGGGGCACCTGGAGCGCAGG 586
Db 1977 CTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTTGGCGCACTGGCTATACGACAGATT 2036
Qy 587 CGACGGGCTGGGCTGTGCGCTTTTTCAGCGGCCACGCGCTGGTGTCTGCTGCGGCTGCGCGG 646
Db 2037 CTCATCCGCTGATCGTCTCTCTTCCATGGCTTTTCTTTCATGATCTTCCAGATTGGAG 2096
Qy 647 TCC-----ACGTGGCGGTGGAGCATCAGCTCCGCGCGCTCCCGT 688
Db 2097 TTCTAGTGTGGACCAACATATGTTGTGTAGCATATACACTGCCACAGCTTCCCGT 2156
Qy 689 GTGCTCTGCTTTCGAGCAGGTTAGGTTTCTGATGAAAGCTACTCTCTTCTCTGAGAGAGG 748
Db 2157 TCATCATTTATTCGAGCAGATTCGTTTGTGTAATGAAGGCCCACTCATTTGTCAGAGAGA 2216
Qy 749 CTGTGCTTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCCCGCCAGTTTCTCCA 808
Db 2217 ACGTCCCTCGGCTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAAATACATACA 2275
Qy 809 G-----CTACCTCTACTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
Db 2276 GTCAACCACTATTGCTACTTCTTATTTGCTCTCTACCTTATCTACCTGTCACAGCTATCCC 2335
Qy 862 AGGAGCCCTATGTCAGGTGGAATTTATGTGGCCAAAGAACTTTGGCCAGGCCCTGGGATGT 921
Db 2336 AGGAATCCCACTGTAAGATGGGTTTATGCTGCTATGAAGTTTGGACAGCTTCTTGTGTGC 2395
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[illegible]

RESULT 7

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US-08-509-187D-2
; Sequence 2, Application US/08509187D
; Patent No. 5834283
; GENERAL INFORMATION:
; APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/509,187D
; FILING DATE: 31-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lampert Hammitte, Ann
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033cpdv
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-509-187D-2

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Query Match	22.9%;	Score 359.8;	DB 2;	Length 4079;
Best Local Similarity	58.0%;	Pred. No. 6.6e-83;		
Matches 722;	Conservative 0;	Mismatches 502;	Indels 21;	Gaps

QY	287	CATCCCTCGGGAAACAGAAAGTTTTCATCATCCGCAAGCTCCCTGCTTGATGAGCTGATGG	346
DB	1808	CACCTCCAGAACAGAAAGATTTTATTTGCAAGCGCTCTCTCTTAGTGAAGTACCTGCTG	1867
QY	347	AGGTGACGCAATTTCCGCACCATCTACCAACATGTTTCATCGCTGGCGTGCTGTCTTCATCA	406
DB	1868	AAGTGACCAACATCAGAACAAATATATCATATGTTTATTTGGCCCTCCTCATCTCTTTATCC	1927
QY	407	TCAGCACCTCGGCATCGACATTCATATGATGAGGGCAGGCTGCTGCTGG--AGTTTGACCT	464
DB	1928	TCAGCACATCTGTAGTAGATTAATCATATGATGAAGGAAGGCTGGTGCTGCAAGTTACGCGT	1987
QY	465	ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGGCCCATGTTTC	523
DB	1988	CTGTCTTATGCATTTTGGCAAAATTTCTACCGTGTGTTGGACCTGGTGATCATGTTC	2047
QY	524	TGTCACCCTGTGGCGCGGTACCAAGCGCTACGGCTGTGGCGCAGGGGCACCTTGAGCGC	583
DB	2048	TGTCTACATTTTCAGTTCCTTATTTCTGTTTCAACATTTGGCGACATGGCTATAGCAAGA	2107
QY	584	AGCGAGGGCCTGGCGTGTGCGCTTTTAGCGGCCACCGCGTGGTGCTCTCGCGGCTGC	643
DB	2108	GTCTCATCGGTGATCCGTTCTCTCTTCATATGGCTTTCTTTTCATGATCTTCCAGATTG	2167
QY	644	CGGTCCACGTGGCG-----TGGAGCATCAGCTCCCGCGGCTCCCGTTGT	690
DB	2168	GAGTTCTAGGTTTGGACCAACATATGTTGTGTTTAGCATATCTCTGCCACAGCTTCCCGG	2227
QY	691	GTCTTGCTCTCGACGAGTTAGTTTCCTGTATGAAGACTACTCTCTCTCGAGAGGCT	750
DB	2228	TTTCATCATTTATCGACAGATCGTTTGTATGAAGGCCACTCATTTGTCAGAGAGAAC	2287
QY	751	GTGCTGGGATCCTTGTGTCACAGAGGTGAGGGATCCAGGCC-----CCCAGTTTCT	805
DB	2288	GTGCTCGGGTACTAATTCAGCTAAGAGAAATCAAGCACTGTTCCAAATACCTACAGTCA	2347
QY	806	CAAGCTACCTCTACTTCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGA	865
DB	2348	ACCAGTATTTGACTTCTTATTTGCTCTACCCCTTATCTACCGTGACAGCTATCCCAAG	2407
QY	866	CGCCCTATCTCAGGTGGAAATATGTGGCCAGAACTTTGGCCAGCCCTGGGATGTGTC	925
DB	2408	ATCCCACTGAAGTGGGGTTATGTGATGAAGTTTGCACAGGCTCTTGGTGTCTTTT	2467
QY	926	TCATGCCCTGCTTCATCCGTGGCGCGCTCTGTGTTCTCTTTTGGCCAAATGAGCGAG	985
DB	2468	TCATATGTGACTACATCTTTGAAGGCTTTGTGGCCCGCTTTGTTTGGAAATATCAACAGG	2527
QY	986	AGCCCTTCAGCACCGCTGCCCTGGTGCTCTCATCTCGATGCCAGCTTGGCAGGCATCT	1045
DB	2528	AGCCCTTCAGCGCTCGTGTTCTGGTGCTATGTGTAATTAAGTCCATCTTGGCAGGTGTC	2587
QY	1046	TCATGCTGCTCATCTTCTTTTGGCTTCTCTCAFTGCTGGCTCAAGCCCTTTGCCGAGA	1105
DB	2588	TGATTTCTTCTCTTACTTTTTTTTGGCTTTTTCGACTGCTGGCTCAATGCCCTTGTCTG	2647
QY	1106	TGCTACGATTTGGACAGAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTCTCCA	1165
DB	2648	TGTTACGCTTTTGTGACAGGATGTTCTATAAGGATTTGTGGAACCTCCACGTCATCTCCA	2707
QY	1166	ACTACTACCGCACTTGGAAAGCTGGTGTCATGACTGGCTGTACAGCTACGTGTATCAGG	1225
DB	2708	ACTATTATAGAACCTGGAAATGTGGTGGTCCATGACTGGCTATATTACTATGCTTACAAGG	2767
QY	1226	ATGGGCTCGGGCTCCTTGGTGGCGCGGGCCGAGGGTAGCCATGCTGGGTGTTCTCTGG	1285
DB	2768	ACTTCTCTGGTTTTTCTCCAAGAGATTCAAAATCTGCTGCCATGTTAGCTGTCTTTGCTG	2827
QY	1286	TCCTCCGACGTGGCCCATAGTATATCTTCTGCTCGTCCCTGGGGTTCTTCTATCCCCGTCA	1345

Db 3008 TCTGTTTATCTCAAGAATGGTATGACGTCGGCACTGTACCT 3052

RESULT 9

PCT-US93-09704A-2

; Sequence 2, Application PC/TUS9309704A

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; NUMBER OF SEQUENCES: 9

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/09704A

; FILING DATE: October 12, 1993

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. SER. NO. 959,950

; FILING DATE: October 14, 1992

; APPLICATION NUMBER: U.S. SER. NO. 121,057

; FILING DATE: September 10, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: LAMPORT HAMMITTE, ANN.

; REGISTRATION NUMBER: 34,858

; REFERENCE/DOCKET NUMBER: DCI-033CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-2700

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4079 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

PCT-US93-09704A-2

Query Match 22.9%; Score 359.8; DB 5; Length 4079;
 Best Local Similarity 58.0%; Pred. No. 6.e-83;
 Matches 722; Conservative 0; Mismatches 502; Indels 21; Gaps 4;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGG 346
 Db 1808 CACCTCCAGAACAGAAAGATTTTATTTGCAAGGCGCTCTCTTAGATGAACCTGCTTG 1867

QY 347 AGGTGCAGCATTTCCGACCATCTACCATGTTTCATCGCTGGCCTGTGTCTTCATCA 406
 Db 1868 AAGTGGACCATCAGAACATATATCATGTTTATTTGCCCTCCTCATCTCTTTATCC 1927

QY 407 TCAGCACCTGGCCATCGACTTCATGATGAGGAGGCTGCTGTGG--AGTTGACCT 464
 Db 1928 TCAGCACACTTGTAGTAGATTACATGATGAAGGAAGGCTGCTGTGCAAGTACGCT 1987

QY 465 ACTG-ATCTTACGCTCGACAGCTGCCATTGGCGCTGTGACCTGGGTGGGTCATCTTC 523
 Db 1988 CTTGCTTATGATTTTGGCAATTTCTTACCGTTGTTTGGACCTGGTGGATCATGTTC 2047

QY 524 TGTCCACCTGTTGGCGCGCTACGAGCGCTACGCGCTGTGGCCAGGGGCACTGGACGC 583
 Db 2048 TGTCTACATTTTCAGTTCCTATTTCTTTCAACATTTGGCGCACTGCTATACGA 2107

QY 584 AGGCGACGGCTGGGCTGTGGCTTTTATAGCGCCACCGCTGTGTCTGCGCGCTGC 643
 Db 2108 GTTCTCATCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATG 2167

QY 644 CGGTCCACGTGGCG-----TGGAGCATCAGTCCCGCGCTCCCGTGT 690
 Db 2168 GAGTTCTAGTTTGGACCAACATATGTTGTGTAGCATATCTGCCACCACTTCCCGG 2227

QY 691 GTCCCTGGTCTTCGAGCAGGTTAGGTTCTGTGATGAAAAGTACTCTCTCTCTGAGAGGCT 750
 Db 2228 TTATCATATTTCGAGCAGATCGTTTGTATGAGGCCACTCATTTGTGAGAGAA 2287

QY 751 GTGCTGGGATCCTTCGTCGACAGAGGTGAGGGATCCAGGCC-----CCAGTTTCT 805
 Db 2288 GTGCTCGGGTACTAATTCAGCTAAGGAAATCAAGCACTGTTCCAAATACATACAGTCA 2347

QY 806 CCAGCTACCTCTACCTCTCTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGA 865
 Db 2348 ACCAGTATTGTACTTCTTATTTGCTCTACCTTATCTACCGTGACAGCTATCCAGGA 2407

QY 866 GCCCTATGTCAGGTGGAATTTATGTGGCAAGAACTTTCGCCAGGCCCTGGGATGTGTC 925
 Db 2408 ATCCCACTGTAAGATGGGTATGTGCTATGAAGTTTGCACAGGTCTTGGTGTCTTT 2467

QY 926 TCTATGCTGCTTCATCTGCGCCGCTCTGTGTCCTGTCCTTCCCAACATGAGCCGAG 985
 Db 2468 TCTATGCTGCTTACATCTTTGAAAGGCTTGTGCGCCCTTGTTCGGAATATCAACAGG 2527

QY 986 AGCCCTTCAGCACCGCTGCCGTGCTCTCTATCTGCTGCACTGCCAGGTGCGCAGCATCT 1045
 Db 2528 AGCCCTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2587

QY 1046 TCATGCTGCTGCTCATCTTCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC 1105
 Db 2588 TGATTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2647

QY 1106 TGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGTGGAACTCAACAGTCTCTTCTCA 1165
 Db 2648 TGTACGCTTTGGTGACAGGATGTTCTATAGGATTTGGTGAACCTCCAGTCTATCTCCA 2707

QY 1166 ACTACTACCGCACTTGGAAAGTGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225
 Db 2708 ACTATTAGAACCTGGAAATGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2767

QY 1226 ATGGCTGCGGCTCCTTGTGCTGCCGCGGAGGCTGAGCATGCTGGGTGTTCTCTG 1285
 Db 2768 ACTTTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 2827

QY 1286 TCTCCGAGTGGCCCATGATATATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1345
 Db 2828 TATCTGCTGTAGTACACAAATATGCTTGGCTGTTTGGTGTGCTGCTGCTGCTGCTGCTG 2887

QY 1346 TCTGATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1405
 Db 2888 TGTTCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2947

QY 1406 CCGGCCCGCATGGAACGCTGCTGATGTGACCATGCTGTTTCTAGGCCAGGAATCCAGG 1465
 Db 2948 AAAAGCCGATTTTGAATGTTCTGATGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3007

QY 1466 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1510
 Db 3008 TCTGCTTTTATTTCTCAAGAAATGGTATGCACTGCGCACTGTACCT 3052

RESULT 10

US-08-121-057-1

; Sequence 1, Application US/08121057

; Patent No. 5484727

; GENERAL INFORMATION:

; APPLICANT: CHANG, TA-YUAN

; APPLICANT: CHANG, CATHERINE C. Y.

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

862	ATCCCACTGTAAGATGGGGTTATGTGTGCTATATGAAGTTTGGACAGGTCCTTTGGTTGGCTTTT	921
926	TCTATGCTCTGCTTCATCTGGCGCGCTCTGTGTCTCTTTCGCAACATGAGCGGAG	985
922	TCTATGTGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTGTTCGGAAATATCAACAGG	981
986	AGCCCTTCAGCACCC 1000	
982	AGCCCTTCAGCGCTC 996	
RESULT 11		
US-08-509-187D-1		
Sequence 1, Application US/08509187D		
Patent No. 5834283		
GENERAL INFORMATION:		
APPLICANT: Chiang, Ta-Yuan and Chang, Catherine C.Y.		
TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase		
NUMBER OF SEQUENCES: 9		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: LAHIVE & COCKFIELD, LLP		
STREET: 28 State Street		
CITY: Boston		
STATE: Massachusetts		
COUNTRY: USA		
ZIP: 02109		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: PatentIn Release #1.0, Version #1.25		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/509,187D		
FILING DATE: 31-JUL-1995		
CLASSIFICATION: 435		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER:		
FILING DATE:		
ATTORNEY/AGENT INFORMATION:		
NAME: Lampert Hammitte, Ann		
REGISTRATION NUMBER: 34,858		
REFERENCE/DOCKET NUMBER: DCI-033cpdv		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: (617)227-7400		
TELEFAX: (617)742-4214		
INFORMATION FOR SEQ ID NO: 1:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 996 base pairs		
TYPE: nucleic acid		
STRANDEDNESS: single		
TOPOLOGY: linear		
MOLECULE TYPE: cdna		
US-08-509-187D-1		
Query Match	8.6%;	Score 134.6; DB 2;
Best Local Similarity	53.1%;	Pred. No. 2.6e-25;
Matches	390;	Conservative 0; Mismatches 324; Indels 21; Gaps
QY	287	CATCCCTGGGGAACAGAAAGTTTTCATATCCGAAAGTCCCTGCTTGATGAGCTCATGG 346
Db	262	CACCTCCAGAACAGGAAAGATTTTTATTCGAAGGGCGCTCTCTCTTAGATGAACCTGCTTG 321
QY	347	AGGTGACAGATTTCCGACCACTCATACCACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406
Db	322	AAGTGGACCAATCAGAACAAATATACATGTTATTGCGCTCCCTCATTCCTTTATTC 381
QY	407	TCACGACCCCTGGCCATCGACTTCATTGATGAGGCGAGGCTGCTGCTGG --AGTTTGACCT 454
Db	382	TCACGACACTGTGTAGATTACATTGATGAAGAGGCTGGTGCCTTGCAAGTTACGCTC 441
QY	465	ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACTGGGTGCCCATGTTTC 523
Db	442	CCTCTCTATGCAATTTGGCAAAATTCCTACCGCTGTTGTTGGACCTGGTGTGATGTTTC 501

;; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

;; NUMBER OF SEQUENCES: 9

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: ASCII Text

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US93/09704A

;; FILING DATE: October 12, 1993

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: U.S. SER. NO. 959,950

;; FILING DATE: October 14, 1992

;; APPLICATION NUMBER: U.S. SER. NO. 121,057

;; FILING DATE: September 10, 1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: LAMPORT HAMMITTE, ANN.

;; REGISTRATION NUMBER: 34,858

;; REFERENCE/DOCKET NUMBER: DCI-033CP

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617) 227-2700

;; TELEFAX: (617) 227-5941

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 996 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: cdna

;; PCT-US93-09704A-1

Query Match 8.6%; Score 134.6; DB 5; Length 996;

Best Local Similarity 53.1%; Pred. No. 2.6e-25;

Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

Qy 287 CATCCCTGGGAAACAGAAAAGTTTTCATATCCCAAGTCCCTGCTTGATGAGCTATGG 346

Db 262 CACCTCCAGAACAGAAAGATTTTATTGCAAGGCGCTCTCTTAGATGAAGTGTG 321

Qy 347 AGGTGCACATTTCCGACCATCTACACATGTTTCATCGTGGCTGTGTCTTCATCA 406

Db 322 AAGTGGACCATCAGAACAAATATACATGTTATTGCGCTCTCTATCTCTTTATCC 381

Qy 407 TCAGCACCTGGCCATGACTTCATTGATGAGGACGCTGCTGCG--AGTTTGACCT 464

Db 382 TCAGCACACTTGTAGTACATTACATTGATGAAGGAGGCTGTGCTGCAAGTTACGCT 441

Qy 465 ACTG-ATCTTCAGCTTCGACAGCTGCCATTTGGCGCTGGTCACTGGTGCCCATGTTTC 523

Db 442 COTGTCTTATGCATTTTGGCAAAATTCCTACCGTTGTTTGGACCTGGTGGATCATGTTCC 501

Qy 524 TGTCACACCTGTGTGGCGCGGTACACAGGCGCTACGCGCTGTGGCGGACGCTGGAGCG 583

Db 502 TGCTACATTTTCAGTTCCCTATTTCTGTTTCAACATTTGGCGACCTGGCTATAGCAAGA 561

Qy 584 AGGCGACGGCGCTGGGCTGTGCGCTTTTATGCGGCCACGCGGTGGTGC-----633

Db 562 GTTCTCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 621

Qy 634 ----TCGGGCGCTCCGCTCCAGCTGGCGCTGGAGCATGACGCTCCCGCGGCTCCCGTTGT 690

Db 622 GAGTTCTAGTTTGGACCAACATATGTTGTTTATGACATATCCTGCCACCACTTCCCGG 681

Qy 691 GTCCCTGGTCTTCGACGAGTTAGTTTCTGATGAAAGACTACTCTCTCTCTGAGAGAGCT 750

Db 682 TTATCATATTTCGACGAGATCGTTTGTATGAGGCCCACTCATTTCTCAGAGAGAAC 741

Qy 751 GTCCCTGGGATCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCC-----CCAGTTTCT 805

Db 742 GTGCCCTCGGTTACTAATTCAGCTAAGGAGAAATCAAGCACTGTTTCCAAATACCTACAGTCA 801

Qy 806 CCAGCTACCTCTACTTCTCTCTGCCCAACACTCATCTACAGGGAGACTTACCTTAGGA 865

Db 802 ACCAGTATTGTACTTCTTATTGTCTTACCTTATCTACCGTGACAGCTATCCAGGA 861

Qy 866 CGCCCTATGTCAGGTGGAATTTATGTGGCCAAGAACTTTGCCAGGCCCTGGGATGTGTC 925

Db 862 ATCCCACTCTAAGATGGGTTATGTGCTATGAAGTTGCACAGGCTTTGGTGTCTTT 921

Qy 926 TCTATGCCCTTCATCTCTGGCGCGCTGTGTGCTCTTGTGCAACATGAGCCGAG 985

Db 922 TCTATGTGTACTACATCTTTTGAAGGCTTTGTGCCCGCTTTTTCGAATATCAACAGG 981

Qy 986 AGCCCTTCAGCACCC 1000

Db 982 AGCCCTTCAGCGCTC 996

RESULT 14

US-09-326-203A-14

; Sequence 14, Application US/09326203A

; Patent No. 644876

; GENERAL INFORMATION:

; APPLICANT: Lassner, Mike

; APPLICANT: Ruezinsky, Diane

; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic

; TITLE OF INVENTION: Acid Sequences

; FILE REFERENCE: 17045/00/WO

; CURRENT APPLICATION NUMBER: US/09/326,203A

; CURRENT FILING DATE: 1999-06-04

; PRIOR APPLICATION NUMBER: 60/088,143

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/108,389

; PRIOR FILING DATE: 1998-11-12

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 1895

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (209)

; OTHER INFORMATION: n at position 209 is unknown

US-09-326-203A-14

Query Match

6.1%; Score 95; DB 4; Length 1895;

Best Local Similarity 58.7%; Pred. NO. 4.9e-15;

Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

Qy 1019 TCCTGTCATGCCAGCTTCCAGGCATCTTCATGCTGCTGCTCATCTCTTTTGCCTTCTCC 1078

Db 913 TCCTGAAGTGGCGGTCCCAATCACCTCATCTGGCTCATCTTCTTACTGGCTCTCC 972

Qy 1079 ATTGCTGGCTCAAGCCCTTTTGGGAGATGCTACGATTGGAGACAGGATGTTTACCGGG 1138

Db 973 ACTCCTGCCTGAATGCGGTGCTGAGCTCATGCTGAGTGTGGAGACCGGGAGTCTTACCGGG 1032

Qy 1139 ACTGGTGGAACTCAACCTCTCTTCCAACTACTACCGCACTTGGAACTGGTGTCTCATG 1198

Db 1033 ACTGGTGGAACTCCGAGTGTCTACCTACTTCTGGCAGAACTGGAACTCCCTGTGCGACA 1092

Qy 1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGCTGCGGCTCTTGTGTGCCCGGCCGAG 1258

Db 1093 AGTGGTGCATCAGACACTTCTACAGGCCCATGCTTCACAC-----GGGCGACGACAGT 1146

Qy 1259 GGGTAGCCATCTGGGTGTGTTCTCTCGCAGTGGGCCCATGAGTATATCTTCTGCT 1318

Db 1147 GGATGGCCAGACAGGGGTGTTCTCTGGCCTCGGCTTCTTCCACGAGTACCTGTGTGAGCG 1206

Qy 1319 TCGTCTGGGGTTTCTTC 1335

Db 1207 TCCCTCTGCGAATGTTTC 1223

RESULT 15
US-09-165-042-2
; Sequence 2, Application US/09165042
; Patent No. 6100077
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165.042
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1976
; TYPE: DNA
; ORGANISM: Yeast
US-09-165-042-2

Query Match 6.1%; Score 95; DB 3; Length 1976;
Best Local Similarity 58.7%; Pred. No. 5e-15;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;
Qy 1019 TCCTGCATGCCACGGTTGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGCCCTTCCTCC 1078
Db 1212 TCCTGAAGCTGGCGTCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGGCTCTTCC 1271
Qy 1079 ATTGCTGGCTCAACCCCTTTCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCCGG 1138
Db 1272 ACTCTGGCTGAATGCCGCTGGCTGAGCTCATGCACTTTGGAGACCGGGAGTTCTACCCGG 1331
Qy 1139 ACTGTTGAACCTCAACGCTCTTCTCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198
Db 1332 ACTGTTGAACCTCCAGTCTGTCACCTACTTTCGCAGAACTGGAACTCCCTGTGCACA 1391
Qy 1199 ACTGCTGTACAGCTACGTGTATCAGATGGGCTGCGGCTCCTTGGTCCCGGCCCGAG 1258
Db 1392 AGTGTGTCATCAGACACTTCTACAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1445
Qy 1259 GGGTAGCCATGCTGGTGTCTTCCCTGGTCTCGGCAGTGGCCCATGAGTATATCTTCTGCT 1318
Db 1446 GATGGCCAGGACAGGGGTGTCTTGGCTCGGCTTCTTCCACGAGTACCTGGTGAGCG 1505
Qy 1319 TCGCTCTGGGTTCTTC 1335
Db 1506 TCCCTCTCGGAATGTC 1522

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Job time : 95 secs

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 14:09:11 ; Search time 141 Seconds
(without alignments)
13148.677 Million cell updates/sec

Title: US-09-918-026a-3

Perfect score: 1569

Sequence: 1 atgagccaggcggggccg.....cttgctctgccatacctag 1569

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 745064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403.6	25.7	418	9	US-09-918-995-33158 Sequence 33158, A
2	391	24.9	399	9	US-09-918-995-33281 Sequence 33281, A
3	387.2	24.7	401	9	US-09-918-995-33355 Sequence 33355, A
4	386	24.6	402	9	US-09-918-995-33444 Sequence 33444, A
5	385.6	24.6	401	9	US-09-918-995-33843 Sequence 33843, A
6	384	24.5	393	9	US-09-918-995-33739 Sequence 33739, A
7	376.2	24.0	401	9	US-09-918-995-33159 Sequence 33159, A
8	350.6	22.3	365	9	US-09-918-995-34424 Sequence 34424, A
9	350.6	22.3	408	9	US-09-918-995-34099 Sequence 34099, A
10	338.2	21.6	383	9	US-09-918-995-35056 Sequence 35056, A
11	138.8	8.8	471	9	US-09-918-995-33288 Sequence 33288, A
12	95	6.1	993	10	US-09-764-853-79 Sequence 79, Appl
13	95	6.1	1411	9	US-10-273-438-1 Sequence 1, Appl
14	95	6.1	1895	9	US-10-157-855-14 Sequence 14, Appl
15	93.8	6.0	542	9	US-09-764-868-587 Sequence 587, App
16	92.4	5.9	774	9	US-09-764-868-279 Sequence 279, App
17	81.4	5.2	447	9	US-09-918-995-29256 Sequence 29256, A
18	81.4	5.2	452	10	US-09-867-701-4664 Sequence 4664, Ap
19	81.4	5.2	1650	9	US-10-273-438-3 Sequence 3, Appl

20	81.4	5.2	1650	9	US-10-273-438-9 Sequence 9, Appl
21	80	5.1	1122	9	US-09-774-639-29 Sequence 29, Appl
22	80	5.1	1122	9	US-09-969-730-58 Sequence 58, Appl
23	79.8	5.1	1766	9	US-10-157-855-15 Sequence 15, Appl
24	79.8	5.1	1766	9	US-10-157-855-16 Sequence 16, Appl
25	70.2	4.5	1572	9	US-10-223-076-17 Sequence 17, Appl
26	67.6	4.3	1181	9	US-10-223-076-12 Sequence 12, Appl
27	57.8	3.7	2099	9	US-10-223-076-11 Sequence 11, Appl
28	55.4	3.5	519	9	US-10-157-855-11 Sequence 11, Appl
29	54.2	3.5	471	9	US-09-918-995-1579 Sequence 1579, Ap
30	53.6	3.4	1964	9	US-10-223-076-14 Sequence 14, Appl
31	52.6	3.4	1537	9	US-10-223-076-4 Sequence 4, Appl
32	52.4	3.3	1446	9	US-10-223-076-6 Sequence 6, Appl
33	52.4	3.3	1512	9	US-10-223-076-8 Sequence 8, Appl
34	50	3.2	1904	9	US-10-223-076-2 Sequence 2, Appl
35	50	3.2	1942	9	US-10-157-855-1 Sequence 1, Appl
36	49	3.1	2090	9	US-10-223-076-10 Sequence 10, Appl
37	47.8	3.0	380	10	US-09-770-791-192 Sequence 192, App
38	45.8	2.9	433	10	US-09-764-853-314 Sequence 314, App
39	43.8	2.8	275	10	US-09-878-574-15694 Sequence 15694, A
40	41.8	2.7	790	9	US-10-123-155-204 Sequence 204, App
41	41.8	2.7	2802	10	US-09-815-242-7720 Sequence 7720, Ap
42	41.2	2.6	2715	9	US-09-712-363-101 Sequence 101, App
43	40.6	2.6	594	9	US-10-123-155-10 Sequence 10, Appl
44	40.6	2.6	1089	10	US-09-866-562-60 Sequence 60, Appl
45	40.6	2.6	1176	10	US-09-866-562-59 Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-918-995-33158
; Sequence 33158, Application US/0918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33158
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33158

Query Match	25.7%	Score	403.6;	DB-9;	Length	418;			
Best Local Similarity	99.0%;	Pred. No.	2.8e-110;						
Matches	406;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1122	CAGGATGTTCTACCGGACTGGTGGAACTCAAGCTCTTCTTCCAACTACTACCGCACTTG	1181						
Db	9	CAGGATGTTCTACCGGACTGGTGGAACTCAAGCTCTTCTTCCAACTACTACCGCACTTG	68						
QY	1182	GAACGTGGTGGTCCATGCTGTACAGTACGTGTATCAGATGGGCTGGCGGTCT	1241						
Db	69	GAACGTGGTGGTCCATGCTGTACAGTACGTGTATCAGATGGGCTGGCGGTCT	128						
QY	1242	TGTCGTCGGGGCCCGAGGGGTACCCATGCTGGGTGTTCCTGCTCTCCGACGTGGGCCA	1301						
Db	129	TGTCGTCGGGGCCCGAGGGGTACCCATGCTGGGTGTTCCTGCTCTCCGACGTGGGCCA	188						
QY	1302	TGAGTATATCTTCTGCTTCGCTCGGGGTCTTCTCATCCCGGTATGCTACTCTTCCT	1361						
Db	189	TGAGTATATCTTCTGCTTCGCTCGGGGTCTTCTATCCCGTTCATGCTGATCTCTTCCT	248						
QY	1362	TGTCATTTGGAGGAATCTTGAATTCATGATGATGATGATGATGATGATGATGATGATGAA	1421						

Db 249 TGTCATGGAGGAATGTTGAACCTTCATGATGACACGCGACCGCGCCGCGCATGGAA 308
QY 1422 CCGTCTGATGTGACCATGCTGTTTCTAGCCAGGAATCCAGGTGAGCTGTACTGCGCA 1481
Db 309 CGTCTGATGTGACCATGCTGTTTCTAGCCAGGAATCCAGGTGAGCTGTACTGCGCA 368
QY 1482 GGAGTGGTAGCCAGCGCGGCGCACTGCCCCCTACCCAGGCAACTTTCTGGG 1531
Db 369 GGAGTGGTAGCCAGCGCGGCGCACTGCCCCCTACCCAGGCAACTTTCTGGG 418

RESULT 2

US-09-918-995-33281
; Sequence 33281, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 1999-01-20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33281
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33281

Query Match 24.9%; Score 391; DB 9; Length 399;

Best Local Similarity 100.0%; Pred. No. 1.6e-106; Indels 0; Gaps 0;
Matches 391; Conservative 0; Mismatches 0;

QY 1122 CAGGATGTTCTACCGGACTGTTGGAATCAACGTCCTTCTCCAACTACTACCGCACTTG 1181
Db 9 CAGGATGTTCTACCGGACTGTTGGAATCAACGTCCTTCTCCAACTACTACCGCACTTG 68
QY 1182 GAACGTGGTGTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
Db 69 GAACGTGGTGTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 128
QY 1242 TGGTCCCGCGCGGAGGGGTAGCCATGCTGGGTGTTCTATCCCGTCATGCTGATCTTCTCCT 1361
Db 129 TGGTCCCGCGCGGAGGGGTAGCCATGCTGGGTGTTCTATCCCGTCATGCTGATCTTCTCCT 248
QY 1422 CCGTCTGATGTGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTGAGCTGTACTGCGCA 1481
Db 129 TGGTCCCGCGCGGAGGGGTAGCCATGCTGGGTGTTCTATCCCGTCATGCTGATCTTCTCCT 1361
QY 1302 TGAGTATATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
Db 189 TGAGTATATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
QY 1362 TGTCATGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1421
Db 249 TGTCATGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 308
QY 1422 CCGTCTGATGTGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTGAGCTGTACTGCGCA 1481
Db 309 CCGTCTGATGTGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTGAGCTGTACTGCGCA 368
QY 1482 GGAGTGGTAGCCAGCGCGGCGCACTGCCCCCTA 1512
Db 369 GGAGTGGTAGCCAGCGCGGCGCACTGCCCCCTA 399

RESULT 3

US-09-918-995-33355
; Sequence 33355, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33355
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33355

Query Match 24.7%; Score 387.2; DB 9; Length 401;

Best Local Similarity 99.0%; Pred. No. 2.1e-105; Indels 0; Gaps 0;
Matches 389; Conservative 0; Mismatches 4;

QY 1122 CAGGATGTTCTACCGGACTGTTGGAATCAACGTCCTTCTCCAACTACTACCGCACTTG 1181
Db 9 CAGGATGTTCTACCGGACTGTTGGAATCAACGTCCTTCTCCAACTACTACCGCACTTG 68
QY 1182 GAACGTGGTGTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
Db 69 GAACGTGGTGTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 128
QY 1242 TGGTCCCGCGCGGAGGGGTAGCCATGCTGGGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 129 TGGTCCCGCGCGGAGGGGTAGCCATGCTGGGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 188
QY 1302 TGAGTATATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
Db 189 TGAGTATATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
QY 1362 TGTCATGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1421
Db 249 TGTCATGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 308
QY 1422 CCGTCTGATGTGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTGAGCTGTACTGCGCA 1481
Db 309 CCGTCTGATGTGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTGAGCTGTACTGCGCA 368
QY 1482 GGAGTGGTAGCCAGCGCGGCGCACTGCCCCCTTACC 1514
Db 369 NGAGTGGTAGCCAGCGCGGCGCACTGCCCCCTTACC 401

RESULT 4

US-09-918-995-33444
; Sequence 33444, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33444
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33444

Query Match

24.6%; Score 386; DB 9; Length 402;

Best Local Similarity 98.7%; Pred. No. 4.9e-105;
Matches 389; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1122 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCCTTG 1181
|||||
Db 9 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCCTTG 68
|||||

QY 1182 GAACGTGGTGCTTACAGCTTACAGCTTACAGTGGCTGCGGCTCCT 1241
|||||
Db 69 GAACGTGGTGCTTACAGCTTACAGCTTACAGTGGCTGCGGCTCCT 128
|||||

QY 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 1301
|||||
Db 129 TGGTCCCGGGCCGAGGGGTAAACCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 188
|||||

QY 1302 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361
|||||
Db 189 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248
|||||

QY 1362 TGTCAATTGGAGGAATGTTGAACCTTCATGATGACGACCGCACCGCCGGCATGGAA 1421
|||||
Db 249 TGTCAATTGGAGGAATGTTGAACCTTCATGATGACGACCGCACCGCCGGCATGGAA 308
|||||

QY 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481
|||||
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368
|||||

QY 1482 GGAGTGGTACGACCGCGCACTGCCCTTAC 1513
|||||
Db 369 GGAGTGGTACGACCGCGCACTGCCCTTAC 400
|||||

RESULT 5
US-09-918-995-33843
; Sequence 33843, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33843
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33843

Query Match 24.6%; Score 385.6; DB 9; Length 401;
Best Local Similarity 99.0%; Pred. No. 6.4e-105;
Matches 388; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1122 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCCTTG 1181
|||||
Db 9 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCCTTG 68
|||||

QY 1182 GAACGTGGTGCTTACAGCTTACAGCTTACAGTGGCTGCGGCTCCT 1241
|||||
Db 69 GAACGTGGTGCTTACAGCTTACAGCTTACAGTGGCTGCGGCTCCT 128
|||||

QY 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 1301
|||||
Db 129 TGGTCCCGGGCCGAGGGAACCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 188
|||||

QY 1302 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361
|||||
Db 189 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248
|||||

QY 1362 TGTCAATTGGAGGAATGTTGAACCTTCATGATGACGACCGCACCGCCGGCATGGAA 1421
|||||
Db 249 TGTCAATTGGAGGAATGTTGAACCTTCATGATGACGACCGCACCGCCGGCATGGAA 308
|||||

QY 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481
|||||
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368
|||||

QY 1482 GGAGTGGTACGACCGCGCACTGCCCTTAC 1513
|||||
Db 369 GGAGTGGTACGACCGCGCACTGCCCTTAC 400
|||||

RESULT 6
US-09-918-995-33739
; Sequence 33739, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33739
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(393)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33739

Query Match 24.5%; Score 384; DB 9; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.9e-104; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0;

QY 1122 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCCTTG 1181
|||||
Db 9 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCCTTG 68
|||||

QY 1182 GAACGTGGTGCTTACAGCTTACAGCTTACAGTGGCTGCGGCTCCT 1241
|||||
Db 69 GAACGTGGTGCTTACAGCTTACAGCTTACAGTGGCTGCGGCTCCT 128
|||||

QY 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 1301
|||||
Db 129 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 188
|||||

QY 1302 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361
|||||
Db 189 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248
|||||

QY 1362 TGTCAATTGGAGGAATGTTGAACCTTCATGATGACGACCGCACCGCCGGCATGGAA 1421
|||||
Db 249 TGTCAATTGGAGGAATGTTGAACCTTCATGATGACGACCGCACCGCCGGCATGGAA 308
|||||

QY 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481
|||||
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368
|||||

QY 1482 GGAGTGGTACGACCGCGCACTG 1505
|||||
Db 369 GGAGTGGTACGACCGCGCACTG 392
|||||

RESULT 7
US-09-918-995-33159

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; Sequence 33159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33159
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33159

Query Match      24.0%; Score 376.2; DB 9; Length 401;
Best Local Similarity 98.7%; Pred. No. 4.1e-102;
Matches 389; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 1181
Db      9 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 68

QY 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTACGTTACAGTGGCTCGGGCTCCT 1241
Db      69 GAACGTGGTGTCCATGACTGGCTGTACAGCTACGTTACAGTGGCTCGGGCTCCT 128

QY 1242 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCCCTCCGCACTGGCCCA 1301
Db      129 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCCCTCCGCACTGGCCCA 188

QY 1302 TGAGTATATCTTCTGCTTCGCTCGTGGGTCTTCTATCCCGTCATGCTGATCTCTTCT 1361
Db      189 TGAGTATATCTTCTGCTTCGCTCGTGGGTCTTCTATCCCGTCATGCTGATCTCTTCT 248

QY 1362 TGTCACTGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGAT 1421
Db      249 TGTCACTGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGAT 308

QY 1422 CGTGTGATGTGGACCATGCTGTTTCTAGCCAGGGAATCCAGGTGAGCTGTACTG 1478
Db      309 CGTGTGATGTGGACCATGCTGTTTCTAGCCAGGGAATCCAGGTGAGCTGTACTG 365

RESULT 9
US-09-918-995-34099
; Sequence 34099, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34099
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-34099

Query Match      22.3%; Score 350.6; DB 9; Length 408;
Best Local Similarity 94.9%; Pred. No. 1.7e-94;
Matches 373; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 1181
Db      15 CCGGATTTTCTACCGGACCTGGGGGAACTCAACGTTCTTCTTCAACTACTACCGCACTTG 74

QY 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTACGTTATCAGGATGGCTCGGGCTCCT 1241
Db      75 GAACGTGGTGTCCATGACTGGCTGTACAGCTACGTTATCAGGATGGCTCGGGCTCCT 134

QY 1242 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCCCTCCGCACTGGCCCA 1301
Db      135 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCCCTCCGCACTGGCCCA 194

QY 1302 TGAGTATATCTTCTGCTTCGCTCGTGGGTCTTCTATCCCGTCATGCTGATCTCTTCT 1361
Db      195 TGAGTATATCTTCTGCTTCGCTCGTGGGTCTTCTATCCCGTCATGCTGATCTCTTCT 254
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; Sequence 33159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33159
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33159

Query Match      24.0%; Score 376.2; DB 9; Length 401;
Best Local Similarity 98.7%; Pred. No. 4.1e-102;
Matches 389; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 1181
Db      9 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 68

QY 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTACGTTATCAGGATGGCTCGGGCTCCT 1241
Db      69 GAACGTGGTGTCCATGACTGGCTGTACAGCTACGTTATCAGGATGGCTCGGGCTCCT 128

QY 1242 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCCCTCCGCACTGGCCCA 1301
Db      129 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCCCTCCGCACTGGCCCA 188

QY 1302 TGAGTATATCTTCTGCTTCGCTCGTGGGTCTTCTATCCCGTCATGCTGATCTCTTCT 1361
Db      189 TGAGTATATCTTCTGCTTCGCTCGTGGGTCTTCTATCCCGTCATGCTGATCTCTTCT 248

QY 1362 TGTCACTGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGAT 1421
Db      249 TGTCACTGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGAT 308

QY 1422 CGTGTGATGTGGACCATGCTGTTTCTAGCCAGGGAATCCAGGTGAGCTGTACTG 1481
Db      309 CGTGTGATGTGGACCATGCTGTTTCTAGCCAGGGAATCCAGGTGAGCTGTACTG 368

QY 1482 GGAGTGTACGACGGGCGGCACTGCCCTTACCC 1515
Db      369 GGAGTGTACG-NCGGGCGCACTTGCCCTTACCC 401

RESULT 8
US-09-918-995-34424
; Sequence 34424, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34424
; LENGTH: 365
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Db 660 ACTGGTGAACCTCCGAGTGTGTCACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 601
QY 1199 ACTGGTGTACAGCTACGTGTATCAGATGGGCTGGGCTCTCTGGTGGCCGGCCCGAG 1258
Db 600 AGTGGTGCATCAGACACTTCTACAGCCATGCTTCGAC-----GGGGCAGCAGCAAGT 547
QY 1259 GGTAGCCATGCTGGTGTCTCTGGTCTCGCAGTGGCCCATGAGTATATCTTCTGCT 1318
Db 546 GGATGGCCAGGACAGGGGTGTTCTGGCCTCGGCCTTCTTCCAGAGTACCTGGTGAGCG 487
QY 1319 TCCTCTGGGGTCTTC 1335
Db 486 TCCCTCTGCGAATGTTTC 470

RESULT 13

US-10-273-438-1
; Sequence 1, Application US/10273438
; Publication No. US2003007275A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT APPLICATION NUMBER: US/10/273,438
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-273-438-1

Query Match 6.1%; Score 95; DB 9; Length 1411;
Best Local Similarity 58.7%; Pred. No. 4.2e-18;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGCATGCCACGTTGCCAGGCATCTTTCATGCTGCTCATCTTCTTTGGCTTCTCTCC 1078
Db - 662 TCCTGAAGCTGGCGTCCCAATCACCTCATCTGCTCATCTTCTTCTACTGGCTCTTCC 721
QY 1079 ATTGCTGCTCAAGCCCTTCCCGAGATGCTACGATTTGGAGCAGAGTGTCTTACCCGG 1138
Db 722 ACTCTGCTGAATGCCGTGGCTGAGTCAATGCAATGCAATGCAATGCAATGCAATGCAATG 781
QY 1139 ACTGGTGAACCTCAACGCTCTTCTCAACTACTACCGCACTTGGAAAGCTGGTGTCCATG 1198
Db 782 ACTGGTGAACCTCCGAGTGTCTGACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 841
QY 1199 ACTGGTGTACAGTACGTGTATCAGGATGGGCTGGGCTCTTGGTGGCCCGGCCGAG 1258
Db 842 AGTGGTGCATCAGACACTTCTACAGCCATGCTTCGAC-----GGGGCAGCAGCAAGT 895
QY 1259 GGTAGCCATGCTGGTGTCTCTGGTCTCGCAGTGGCCCATGAGTATATCTTCTGCT 1318
Db 896 GGATGGCCAGGACAGGGGTGTTCTGGCCTCGGCCTTCTTCCAGAGTACCTGGTGAGCG 955
QY 1319 TCCTCTGGGGTCTTC 1335

Db 956 TCCCTCTGCGAATGTTTC 972

RESULT 14

US-10-157-855-14
; Sequence 14, Application US/10157855
; Patent No. US20020170091A1
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael W.
; APPLICANT: Ruzinsky, Diane M.
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 16516.158
; CURRENT APPLICATION NUMBER: US/10/157,855
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 09/326,203
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (209)
; OTHER INFORMATION: n at position 209 is unknown
US-10-157-855-14

Query Match 6.1%; Score 95; DB 9; Length 1895;
Best Local Similarity 58.7%; Pred. No. 4.7e-18;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGCATGCCACGTTGCCAGGCATCTTTCATGCTGCTCATCTTCTTTGGCTTCTCTCC 1078
Db 913 TCCTGAAGCTGGCGTCCCAATCACCTCATCTTCTTCTACTGGCTCTTCC 972
QY 1079 ATTGCTGCTCAACGCTTTCGCGAGATGCTACGATTTGGAGCAGAGTGTCTTACCCGG 1138
Db 973 ACTCTGCTGATGATGCGTGGCTGAGCTCATGCAAGTTGGAGCCGGAGTTTACCCGG 1032
QY 1139 ACTGGTGAACCTCAACGCTCTTCTCAACTACTACCGCACTTGGAGCAGTGGTGTCCATG 1198
Db 1033 ACTGGTGAACCTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 1092
QY 1199 ACTGGTGTACAGCTAGCTATCAGATGGGCTGGGCTGCTTGGTGGCCCGGCCGAG 1258
Db 1093 AGTGGTGCATCAGACACTTCTACAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1146
QY 1259 GGTAGCCATGCTGGTGTGTTCTCTGGTGTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318
Db 1147 GGATGGCCAGGACAGGGGTGTTCTTGGCCTCGGCCTTCTTCCAGAGTACCTGGTGAGCG 1206
QY 1319 TCCTCTGGGGTCTTC 1335
Db 1207 TCCCTCTGCGAATGTTTC 1223

RESULT 15

US-09-764-868-587
; Sequence 587, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

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; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 587
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (377)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (397)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (441)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (507)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-587
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Query Match          6.0%; Score 93.8; DB 9; Length 542;
Best Local Similarity 58.8%; Pred. No. 6.6e-18;
Matches 183; Conservative 0; Mismatches 122; Indels 6; Gaps 1;

Qy 1019 TCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTCATCTTCTTGGCCTTCCCTCC 1078
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 54 TCCTGAAGCTGGCGTCCCAATCACCTCATCTGGCTCATCTTCTTACTGGCTCTTCC 113

Qy 1079 ATTGCTGCTCAACGCCCTTGGCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 114 ACTCCTGCTGAATCCGCTGAGCTCATGCAGTTTGGAGACCGGGAGTTCTACCGGG 173

Qy 1139 ACTGCTGGAACCTCAACGCTTCTCCAACTACTACCGCACCTTGGAAACGTTGGTGCCATG 1198
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 174 ACTGCTGGAACCTCCAGTCTGTACCTACTTCTGGCAGAACTGGAAACATCCCTGTGCACA 233

Qy 1199 ACTGCTGTACAGCTACGTTATACAGATGGGCTCCGGCTCCTTGGTCCCGGGCCCGAG 1258
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 234 AGTGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCGACGCAAGT 287

Qy 1259 GGGTAGCCATGCTGGTGTCTTCTGGTCTCCGGCTCCGGCAGTGGCCCATGATATATCTTCTGCT 1318
    || | |||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 288 GGATGCCAGGACAGGGGTGTTCTTGGCCTGGGCTTCTTCCACGAGTACCTGGTGAGCG 347

Qy 1319 TCGTCTCTGGG 1329
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Db 348 TCCCTCTGGCG 358
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Search completed: April 30, 2003, 15:30:40
Job time : 152 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	402.4	25.6	799	13	BI222037	BI222037 602935989
2	335.8	21.4	563	10	BE236762	BE236762 145578 MA
3	298.2	19.0	778	13	BG920709	BG920709 602824607
4	281.6	17.9	705	12	BG105735	BG105735 602311957
5	272.6	17.4	992	12	BG674469	BG674469 602620487
6	268	17.1	840	12	BG529751	BG529751 602560822

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source
1. 799
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:509063"
/clone_lib="NCI CGAP L19"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: liver; Vector: PCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 176 a 217 c 247 g 158 t
ORIGIN
Query Match 25.6%; Score 402.4; DB 13; Length 799;
Best Local Similarity 78.7%; Pred. No. 1.8e-83;
Matches 524; Conservative 0; Mismatches 126; Indels 16; Gaps 3;

QY 28 CTGCAGAGACAGAAGGCTGGGAGGGGAGCGGCGCAACCCCTGT---GGAGATGGA 84
DB 133 CTTCCGAGGAGAGAAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 192
QY 85 AACCTGAGACGAC-AGAGCCCGGACTGTGTACAAATGACACCGACACATGGAGCTCT 143
DB 193 AACGCAAGACACTTGAACCCAGACTTGGTGAATGGACTGACATATGGAGGCTGT 252
QY 144 GAAGGCACAAATTCGTGAGCAAGCGAGGAGCAACTGAGGGAGCTGCTGGATCGGCCAT 203
DB 253 GAAGACACAGTTCTGGAGCAACACAGAGAGATTGGCAGAGCTGTGGATCGGCCCT 312
QY 204 GCGGAGGCTATACAAATCCATCCATCAAGACAAACCTCTGCCGCCACCTCCCCAGG 263
DB 313 ATGGGAGGCTATGCAAGCTTACCCAAACAGACAGACCTCTTCCCTCCGCTCCCGACA 372
QY 264 TTCCTTGAGCAGACCCAGGAGCCTCCCTGGGAAACAGAAAGTTTTCATATCGGCAA 323
DB 373 TTCTACAAAGAACCCAGAGATTACACCTTGGAAACAGAAAGTTTTCATACCCGCAA 432
QY 324 GTCCTCTGCTGATGAGCTGATGAGGTGCAGCATTTCCGACCATCTACACATGTTTAT 383
DB 433 GTCACATGATGAGCTAATGAGGTGCAACATTTCCGAACCATCTACACATGTTTAT 492
QY 384 CGCTGGCTGTGTCTTATCATCATGACACCCCTGGCCATCGACTTCAATGATAGGCGAG 443
DB 493 AGCGGGCTATGCTGCTGATCATGACACCCCTGGCCATCGACTTCAATGATAGGCGAG 552
QY 444 GCTGCTGCTGAGTTTCACTACTGATCTTCACTTCCGACAGCTGCGCATTTGGCGTGT 503
DB 553 GTTATGCTGAGTTTCACTACTTCTTCTTCACTTCCGACAGCTGCCCTTGGCGTGT 612
QY 504 GACCTGGTGCCCATGTTTCTGTCACCCCTGTTGGCCCGCTACAGGCCCTACGGCTGTG 563
DB 613 GACCTGGGTTCCCATGTTCTGCTAGGCTCTAGTCCCTTACGACAGCCCTGTGGCTGTG 672
QY 564 GGCCA-----GGGCACTGAGCAGCGGCGGCGGCTGGCGTGTGCGCTTTT 611
DB 673 GGCCAGGCGCGCGCTGGGGTGCTGGATGCTGGGGCGGCGGCTGGCGTGTGCTGCT 732
QY 612 AGCCGCGCCACCGCTGTGTCTGCTGCGGCTGCCGGTCCACGTGGCGCTGGAGCATCAGCT 671
DB 733 GGCTGCCACGCTGTGTGCTCTCGCTCCTGCCGCTGACGCTGTCAGTGGAGGCTTGAGCT 792
QY 672 CCGGCC 677
DB 793 TCCGAC. 798.

RESULT 2
LOCUS BE236762 563 bp mRNA linear EST 25-APR-2001
DEFINITION 145578 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE236762
VERSION BE236762.1 GI:9021480

KEYWORDS SOURCE ORGANISM EST.
COW. Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 563)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Petea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001).
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAG
Plate: 55 row: 0 column: 15
Seq primer: ATTTAGTGACACTATAG.
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/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
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/lab_host="DH10B"
/Note="Vector: PCMV SPORT6; Site:1: NotI; Site:2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT 129 a 160 c 170 g 103 t 1 others
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Query Match 21.4%; Score 335.8; DB 10; Length 563;
Best Local Similarity 85.6%; Pred. No. 5.9e-68;
Matches 373; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 82 GGAACACCTGAGACGACAGAGCCCGGAGCTTGGTACAATGGACCCGACACATGGAGGCT 141
DB 128 GGAACCGGAGGTGCACAGAGGCCAGATTTGGTCAATGGACCCAGCATATGACGCT 187
QY 142 GTCAAGGCACATTTCTGGAGCAAGCGGACAGCACTGAGGAGCTGCTGGATCGGCGC 201
DB 188 GTAAGACACAGTTGTGGAGCAAGCGGAGGCCAGCTGATGGAGCTGCTGGATGAGGCC 247
QY 202 ATCGGGAGGCTATACAATCTTACCCTACCAAGACAAACCTCTGCCCCACCTCCGCCCA 261
DB 248 ATGTGGAGCGAGTTCAAGCTTACCCTACCAAGACAGACAGACAGCTCCGCTCCCTCCA 307
QY 262 GGTTCCTTGACAGGACCCAGGAGCCATCCCTGGGAAACAGAAAGTTTTCATCATCCGC 321
DB 308 GACTCCTTGGCAAGACCCCGGAGCGCTCCCTGGGAAAGGAAAGTTTTCATCATCCGC 367
QY 322 AGTCCCTGCTGATGAGCTGATGGAGGTGACGATTTCCGACCATCTACCATGCTTC 381
DB 368 AGTCCCTGCTTGACGAGCTGATGGAGGTGCGGAGCTTCCGACCATCTACCATGCTTC 427
QY 382 ATCGCTGGCCTGTGTCTTTCATCATCAGCACCCCTGGCCATCGACTTCAATGATGAGGC 441
DB 428 GTCCGCGGCTGTGTCTTTCATCATCAGCACCCCTGGCCATCGACTTCAATGATGAGGC 487
QY 442 AGGCTGCTGTGGAGTTTGACCTACTGATCTTACGTTTCAGCTTCGACAGCTGCCATGGCGCTG 501
DB 442 AGGCTGCTGTGGAGTTTGACCTACTGATCTTACGTTTCAGCTTCGACAGCTGCCATGGCGCTG 501

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BASE COUNT 139 a 155 c 153 g 258 t
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Best Local Similarity 64.2%; Pred. No. 3.1e-55;
Matches 439; Conservative 0; Mismatches 244; Indels 1; Gaps 1;
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D 1 CTACCGTGACAGTATCCCAAGGAATCCCACTGTAAGATGGGTATGTGCTATGAAGTT 60
QY 903 TGCCAGGCGCTGGGATGTGTCTATGCTCTTATCCTGCTGGCCGCGCTCTGTCTTC 962
D 61 TGCACAGCTTTTGGTGTCTTTTATGTGTACTACATCTTTGAAGGCT-TGTGCCCC 119
QY 963 TGTCTTTGCCAATGACGAGCGAGCCCTCAGACCCGCTGCTGCTCTCTATCT 1022
D 120 CTTGTTCCGAATATCAACAGGAGCCCTCAGCGCTGTGTCTGCTCTATGTATT 179
QY 1023 GCATGCCAGCTTGCAGGATCTTATGCTGCTCATCTTCTTGGCTTCTCCTCAT 1082
D 180 TAATCCTATCTTGCAGGTGTGTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 239
QY 1083 CTGCTCAAGCCCTTTCCGAGATGCTACGATTTGGAGACAGGATGTTTACCGGACTG 1142
D 240 CTGCTCAATGCCCTTGTCTGAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGAT 299
QY 1143 GTGGAATCAACGCTCTTCCCACTACTACCGCACTTGGAACTGTGTGCTCATGACTG 1202
D 300 GTGGAATCCACGCTACTACTCCAACTATATAGAACTGGAATGTGTGCTCATGACTG 359
QY 1203 GCTGTACAGCTACGTATCAGGATGGCTGCGGCTCCTTGGTGCCGCGCCGAGGGT 1262
D 360 GCTATATCTACTGCTTACAGGACTTCTCTGCTTTTCTTCTTCTTCTTCTTCTTCT 419
QY 1263 AGCATGTGGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
D 420 TGCCATGTAGCTGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 1323 CTGGGCTTCTTATCCCGCTCATGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1382
D 480 CTGAGCTTTTCTATCCCGTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 539
QY 1383 CTTCATGATGATGACGAGCCAGCCGCGGCGGATGGAACGTGCTGATGTGGACCATGCT 1442
D 540 CTTCATGCTCAATGATAGTCAAGAAACCGGATTTGGAATGCTTCTGATGTGGACTTCTCT 599
QY 1443 GTTCTAGCCAGGAATCCAGGTACGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 1502
D 600 TTCTTGGGCAATGAGTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
QY 1503 CTGCCCTTACCCAGCAACTTT 1526
D 660 CTGCTCTGAAATCCACATTT 683
RESULT 5
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LOCUS 602620487f1 NCI_CGAP_Skn3 Homo sapiens cdna clone IMAGE:4746069 5',
DEFINITION mRNA sequence.
ACCESSION BG674469
VERSION BG674469.1 GI:13905865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 992)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10593 row: n column: 22
High quality sequence stop: 828.
Location/Qualifiers
1..992
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/clone="IMAGE:4746069"
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 199 a 216 c 231 g 346 t
ORIGIN

Query Match 17.4%; Score 272.6; DB 12; Length 992;
Best Local Similarity 63.2%; Pred. No. 4.6e-53;
Matches 419; Conservative 0; Mismatches 244; Indels 0; Gaps 0;
QY 901 TTGGCCAGCCCTGGGATGTGTCTATGCTGCTTCTCATCTGCTGCGCCGCTCTGTGT 960
D 2 TTGGCACAGTCTTGGTGTCTTTTCTATGTACTACATCTTTGAAAGGCTTTGTGC 61
QY 961 CTTGTCTTTCCAAATGAGCCGAGAGCCCTTCAGCACCCGCTGCTGCTGCTCTATC 1020
D 62 CCCTGTTTGGGAATATCAACAGGAGCCCTTCAGGCGCTGCTGCTGCTGCTGCTGTA 121
QY 1021 CTGCATGCCAGCTTGGCAGCATCTTCATGCTGCTGCTCTCTCTCTCTCTCTCTCT 1080
D 122 TTTAACTCCATCTTGCAGGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 181
QY 1081 TGTGCTCAACGCTTTGCCAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1140
D 182 TGTGCTCAATGCCCTTGTGAGATGTTACGCTTTTGGTACAGGATGTTCTATAAGGAT 241
QY 1141 TGTGGAACCTCAAGCTTCTTCTCCACTACTACCGCACTTGGAACTGGTGGTCCATGAC 1200
D 242 TGTGGAACCTCCAGCTCATCTCCAACTATATAGAACCTGGAATGTGGTGGTCCATGAC 301
QY 1201 TGGCTGTACAGTACGCTGTATCAGGATGGCTGCGGCTCCTTGGTGGCCGCGCGAGGG 1260
D 302 TGGCTATATTACTATGCTTACAAGGACTTTCTCTGGTCTTCTCCAAAGAGATTCAAATCT 361
QY 1261 GTAGCCATGCTGGGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
D 362 GCTGCCATGTAGCTGCTTTTGTGTATCTGCTGTAGTACACGAATATGCTTGGCTGTT 421
QY 1321 GTCTGGGTTCTTCTATCCGCTCATCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
D 422 TGCTTGAGCTTTTCTATCCGCTGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 481
QY 1381 AACTTCATGATGATACAGGAGCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1440
D 482 AACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
QY 1441 CTGTTCTTAGCCAGGGAATCCAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
D 542 CTTTCTTGGCAATGAGTCTTACTCTGCTTTTATTTCTCAAGAATGATGATGATGATGATGAT 601
QY 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
D 602 CACTGCTCTGAAAAATCCCAATTTTGAATATGTCGCGCCACGCTTCTCTGACTGT 661
QY 1561 CAT 1563

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Db 662 CGT 664

RESULT 6
BG529751
LOCUS
DEFINITION 602560622F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698748 5',
mrna sequence.
ACCESSION BG529751
VERSION BG529751.1 GI:13521288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LICM1529 row: k column: 05
High quality sequence stop: 764.
Location/Qualifiers
1. .840
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/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattcgcc); Site_2: SfiI (ggccattcgcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGCGCCGACATG-dt(30)BN-3'.
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 163 a 195 c 178 g 304 t
ORIGIN

Query Match 17.1%; Score 268; DB 12; Length 840;
Best Local Similarity 63.4%; Pred. No. 5.1e-52;
Matches 460; Conservative 0; Mismatches 260; Indels 6; Gaps 3;

Qy 811 TACCTCTACTTCCCTCTCTGCGCCACACTCATCTACAGGAGACTTACCCTAGGAGCC 870
Db 12 TATTTGTACTTCTTATTTGCTCTTACCCTTATCTACCGTGACAGCTATCCCAGGAATCCC 71

Qy 871 TATGTACAGTGAATATATGTGCGCCAAAGAACTTTGCGCCAGGCCCTGGAGTGTGCTCTAT 930
Db 72 ACTGTAAAGTGGGTATGTGCTATGAAGTTTGCACAGGCTTTGGTTGCTTTTCTAT 131

Qy 931 GCCTGCTTTCATCTGCGCGCCCTGCTGCTTCTGCTTTGCGCAACATGAGCCGAGGCC 990
Db 132 GTGTACTACATCTTTGAAGGCTTTGTGCCCCCTTGTTCGGAATATCAACAGAGGCC 191

Qy 991 TTCAGCACCCGCTGCTGCTCTCTATCTGTCATGCCATGCCAGTTCGCCAGGATCTTCATG 1050
Db 192 TTCAGCGCTCGTGTCTGCTCTATGTGTATTTAACTCCATCTTGCAGGTGTGCTGAT 251

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Qy 1051 CTGCTGCTCA-TCTTCTTTGCTTCTCCATTTGCTGGCTCAACGCTTTGCGAGATGCT 1109
Db 252 CTCCTCTTACTTTTCTTTGCTTCTTTCATCTGCTGGCTCAATGCTTTGCTGAGATGT 311

Qy 1110 ACGATTGAGACAGAGATGTTCTACCGGACTGGTGGAACTCAAGCTCTTCTCCAATA 1169
Db 312 ACGTTTGGTGACAGATGTTCTATAAGGATTTGGTGGAACTCCAGCTCATACTCCAATA 371

Qy 1170 CTACCGCACTTTGGAACGCTGGTGGTCCATGACTGGCTGTACAGCTACGTTGATCAGGATGG 1229
Db 372 TTATAGAACCTGGAAATGGTGGTCCATGACTGGCTATATTACTATGCTTACAAGGACTT 431

Qy 1230 GCTCGGCTCTCTGCTGGTCCCGGCGGAGGAGGTAGCCATGCTGGGTGTTGCTGCTC 1289
Db 432 TCTCTGGTTTCTCCAGAGATTCAAATCTGCTGCCATGTTAGCTGCTTTGCTGTATC 491

Qy 1290 CGCAGTGGCCCATGATATATCTTCTGCTGCTGCTGGGTTCTTCTATCCCGTCACTGCT 1349
Db 492 TCGTGTAGTACACGAATATGCTTGGCTGTTGCTTGGCTTCTTCTATCCGCTGCTCT 551

Qy 1350 GATACTCTTCTCTGCTGCTGAGGAGTCTTGAACCTTCATGATGATGATGATGATGATGAT 1408
Db 552 CGTGTCTTCTCATGTTCTTGTGAATGGCTTCAACTTCATGTCATATGATGTCGACACA 611

Qy 1409 GCCCGCATGGAACGCTGCTGATGCGACCATGCTCTTTCTAGGCCAGGAA-----TCCAG 1464
Db 612 AGCCGATTGGAATGCTGCTGATGCGACTTCTCTTTCTTGGCAATGGAGCTCTTACCT 671

Qy 1465 CTCAGCTGTACTGCTGCGAGAGTGTGACGAGGCGGACTGCCCCCTTACCCAGGCAACT 1524
Db 672 CTGCTTTTATTTCTCACGAAATGGTATGACGCTGACGCTGCTCTCTCTCTCTCTCTCTCT 731

Qy 1525 TTCTGG 1530
Db 732 TTTTGG 737

RESULT 7
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LOCUS AL527439 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC021YJ22 5
DEFINITION prime, mRNA sequence.
ACCESSION AL527439
VERSION AL527439.1 GI:12790932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 893)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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1. .893
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/clone_lib="LTI_NFL003_NBC3"
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/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life

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Qy	902	TTGCCACAGCCCTGGGATGTGTGCTCTATGCTGCTTCACTCTGGGCGCCCTCTGTGTTC	961
Db	13	TTGCACAGGCTTTGGTTGGTTCTTTCTATGCTGCTACTACATCTTTGAAAGGCT-TGTGCC	71
Qy	962	CTGTCTTTGGCAACATGAGCGGAGAGCCCTTCAGACACCGCTGCCCTGGTGTCTCTATGCC	1021
Db	72	CTTTGTTTCGGATATCAACACAGGAGCCCTTCAGCGCTCGTGTCTGGTCTATGTGTAT	131
Qy	1022	TGATGCCACGTTTGGCAGGACATCTTCATGCTGCTGCTCATCTCTTTGCCCTTCTCCCAT	1081
Db	132	TTAACTCCATCTTTGGCCAGGTGTGCTGATCTCTCTCCCTTACTTTTTTTGGCCTT-TTGCACT	190
Qy	1082	GCTGGCTCAACGCTTTTGGCGAGATGCTACGATTTTGGACACAGGATGTTCTACCGGCACT	1141
Db	191	GCTGGCTCAATGCTTTTGGCTGAGATGTTACGCTTTTGGTGACAGGATGTTCTATAAGGAT	250
Qy	1142	GGTGGAACTCAAGCTCTCTTCCAACTACTACCGCACTTTGGAACGCTGGTGGTCCATGACT	1201
Db	251	GGTGGAACTCCACGCTCATCTCCAACTATTATAGAACCTGGAATGGTGGTCCATGACT	310
Qy	1202	GGCTGTACAGCTACGTGTATACAGATGGGCTGGGGCTCTCTGGTCCCGGGGCCGAGGGG	1261
Db	311	GGCTATATTAATGCTTTACAAGGACTTCTCTGGTGTCTTCTGCTTTTCTCCAAGAGATTC	370
Qy	1262	TAGCCATGCTGGGTGTCTTCCCTGGTCTCCGCACTGGCCCATGAGTATATCTTCTGCTTCG	1321
Db	371	CTGCCATGTTAGCTGTCTTTGGTGTATCTGCTGTAGTACACGAATATGCTTTGGCTGTTT	430
Qy	1322	TCCTGGGGTTCTTCTATCCCGTCTATGCTGATCTCTCTCTGCTCATTTGGAGGAATGTTGA	1381
Db	431	GCCTGAGCTTTTCTATCCCGTCTCTTCTGCTCTCTCATGTTCTTGAATGGCTTTCA	490
Qy	1382	ACTTCATGATGATACACAGCGACCGCGCCCGGCAATGGAACGCTGCTGATGTGGACCATGC	1441
Db	491	ACTTCATGTCATGATAGTTCGGAAGAAAGCCGAAATTTGGAATTTCTGATGTGGACTTCTC	550
Qy	1442	TGTTTCTGAGCCAGGAATCCAGTTCAGCTGTACTGCCAGAGTGGTACGCACGCGCGC	1501
Db	551	TTTCTTGGGCAATGAGTCTTACTCTGCTTTTATCTCAAGANTGGTATGCACGCTCAGC	610
Qy	1502	ACTGCCCTTACCCACAGCACTTTCTGG	1530
Db	611	ACTGCTCTCTGAAAAATCCACATTTTGG	639
RESULT	10		
LOCUS	AI049480		
DEFINITION	ub37611.r1 Soares_thymus_2Nbmt Mus musculus cdna clone IMAGE:1379948 5', similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN); gb:L42293 Mus musculus acyl-coenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence.		
ACCESSION	AI049480	731 bp	linear
VERSION	AI049480.1	GI:3297767	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;		
	1 (bases 1 to 731)		
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,		
	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,		
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,		
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
	Waterston,R.		
TITLE	The WashU-HMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800		

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:902416

Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 313.

FEATURES

BASE COUNT	ORIGIN
133 a	189 c 177 g 232 t

BASE COUNT	133 a	189 c	177 g	232 t	ORIGIN
Query Match	15.4%	Score 241.6;	DB 9;	Length 731;	
Best Local Similarity	63.9%	Pred. No. 7.2e-46;			
Matches 381;	Conservative 0;	Mismatches 214;	Indels 1;	Gaps 1;	
Qy	936	CTTCATCTCGGGCGCCTCTGTTCTGTTCTTTGCCAACATGACGGCAGAGCCCTTCAG	995		
Db	10	CTACATCTTTGAGAGACTCTGTGCCCACTATTCGGGAATATCAACAGGAGCCCTTCAG	69		
Qy	996	CACCGTGCCCTGGTGTCTCTATCCTGCATGCCACGTGGCAGGCACTTTTCATGCTGCT	1055		
Db	70	TGCTCGTGTCTGTCCTGTGTGTTAACTCCATCTTGCCAGGTGCTTTGATACGTT	129		
Qy	1056	GCTCATCTTTTGGCTTCCTCCATTTGCTGCTCAAGCCCTTTGCCGAGATGCTACGATT	1115		
Db	130	CTTTTCGTTCTTGGCTTTTGGCACTGCTGCTCAATGCCTTTGTGTGAGATGTTACGCTT	189		
Qy	1116	TGGGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCG	1175		
Db	190	TGGTGACAGGATGTTTATAGGACTGGTGGAACTCTACATCATACTCCAACACTACAG	249		
Qy	1176	CACTTGGAACGTGGTGTCATGACTGGCTGTACAGCTACGTGTATACAGGATGGGCTGG	1235		
Db	250	GACCTGGAACGTGGTGGTGACAGACTGGCTCTACTACTATGTTTACAAGACCTGCTGTG	309		
Qy	1236	GCTCCTTGGTGCCCGGCGGAGGGTAGCCATGCTGGGTGTGTTCTTGGTCTCCGCGACT	1295		
Db	310	GTTTTTCGAAAGAGGTTCAATCTGCCCGCACTGCTGGCCGCTTTCGGCCCTCTCGGCTGT	369		
Qy	1296	GGCCCATGAGTATATCTTCTGCTCGTCTGGGTCTTCTATCCCGTCATGCTGATACT	1355		
Db	370	GGTGACAGATGCCCCTCGCCATCTGCTGAGTTACTTCTACCGGGTGTCTTCTGCTGCT	429		
Qy	1356	CTTCCTTGTTCATTTGAGGAAATGTTGAACATTCATATGATGATGATGACAGC-GCACC	1414		
Db	430	CTTCATGTTCTTTGGAATGGCTTTTACTTCACTATTTGTACGACAGCTGGGAAAGGCCAA	489		
Qy	1415	CATGNACTGCTGATGTGGACCATGCTTTTCTAGGCGAGGAATCCAGGTCAGCCTCT	1474		
Db	490	TCCTGGACATCATGGTTTGGGGTCTCTCTGCTGGGCTATGGATCATCTGCTGTTTT	549		
Qy	1475	ACTGGCAGGAGTGTACGACAGCGGCGCACTGCCCCCTTACCCCCAGGCACTTTCTGG	1530		

Db 550 ATTCTCAAGAGTGGTATGSCCGCCAGCACTGTCTCTGAAGAACCTACATTTCGG 605

RESULT 11
AU099137
LOCUS
DEFINITION
AU099137 300 bp mRNA linear EST 05-APR-2001
AU099137 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP20912 similar to Homo sapiens acyl coenzyme A:cholesterol
acvltransferase 2 mRNA. mRNA sequence.

ACCESSION AU099137
 VERSION AU099137.1
 KEYWORDS EST.
 SOURCE human.

Source: Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 300)

AUTHORS

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata,
K., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo
. . . , Suwama, A. and Sugano, S.

TITLE
In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by

JOURNAL
Unpublished (2001)
Oligo-capping method

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, S. Construction and characterization of a full length, 5'-end-anchored cDNA library. *Gene* 200 (1-2), 149-152.

FEATURES
SOURCE

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source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP20912"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT
78 a 79 c 108 g 35 t

```

BASE COUNT	78 a	79 c	108 g	35 t
ORIGIN				
Query Match		15.3%	Score 240;	DB 9; Length 300;
Best Local Similarity		100.0%;	Pred. No. 1.le-45;	
Matches	240.	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	ATGGAGCCAGGGGGCCCGTCTGCGTCTGCAGAGGACAGAGGGCTGGGAGGGGAGCGG	60
51	ATTCGACCGTACCGGGCCCGCTGCGCTGCGTGCACAGAGGCGTGGCAGGAGGAGCGG	120	

D8 b1 ATGGAGCCAGGCGGGGCCCTGCACGAAGATCAAA 120
c1 AGCGCCGACCGCCTGTTCACACACAGCGCCGACATTGGTACAA 120

61 GAGCGCAACCCCTGTGGAGATGGAAACACTGAGACGCACAGAGCCCCCAGAC 120
QY |||||
180

Db 121 GAGCGCAACCTGAGAGATGGAAACACTGAGAGCGCACAGAGCCCCCGGACATGGTACATA 100

QY
121 TGGACCCGACACATGGAGGCTGTGAAGGCACAATTGCTGGAGCAAGGCCAGGGACAACTG 180

QY
121 TGGACCCGACACATGGAGGCTGTGAAGGCACAATTGCTGGAGCAAGGCCAGGGACAACTG 180

Db 181 TGGACCCGACACATGGAGGCTGTGAAGGCACAATGCTGGAGCAAGCGAGGGACAAC TG 240

QY 181 AGGGAGCTGCTGGATCGGGGGCATGCGGGAGGGCTATACAATCTTACCCATCACAGACAAA 240

Db 241 AGGGAGCTGCTGGATCGGGGGCCATGCGGGAGGCTATACAATCTACCCATCACAGACAAA 300

RESULT 12
BG500675

LOCUS	BC500675	846 bp	mRNA	linear	EST 27-MAR-2000
DEFINITION	602547068f1 NIH_MGC_60 Homo sapiens CDNA clone IMAGE:4669480 5', mRNA sequence.				

ACCESSION BG500675
VERSION BG500675.1 GI:13462192
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 846)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DPV
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1481 row: g column: 17
High quality sequence stop: 684.
Location/Qualifiers
1. 846

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:4669480"
/clone_lib="NIH_MGC_60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pONR-LIB (Clontech);
Site.1: Sf11 (ggcgccctgcgc); Site.2: Sf11 (ggcgccatgagcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."
163 a 197 c 184 g 302 t

Query Match 15.2%; Score 238.8; DB 12; Length 846;
Best Local Similarity 63.2%; Pred. No. 3.5e-45;
Matches 432; Conservative 0; Mismatches 247; Indels 5; Gaps 4;

QY 811 TACCTCTACTCTCTCTGCCCAACATCTACAGGAGACTTACCCTAGGAGCGCC 870
Db 13 TATTTGTACTCTTATTTGCTCCTACCCCTATCTACCGTACAGCTATCCAGGATCCC 72
QY 871 TATGT-CAGGTGGAATATGTGGCCAAAGAACTTTGCCCGGCCCT--GGGATGTGTGTC 927
Db 73 ACTGTGAAGATGGGTATGTGCTATGAACGTTTGCACAGCTCTCTGTTGCTTTTC 132
QY 928 TATGCGTCTTATCTGCGGCCCTCTGTCTCTGCTTTGGCCAAATGAGCCGAGAG 987
Db 133 TATGTGTACTACATCTTTTGAAGAGCTTTGTGCCCCCTTTGCGGAATATCAACAGAG 192
QY 988 CCCTTCAGACCCGTCGCTCTCTATCTCCTG-CATGCCACGTTGCCAGGATCTT 1046
Db 193 CCCTTCAGCGCTCGTCTTGTGCTCTATGTTGTTAACTCCATCTTCCCGAGGTGCT 252
QY 1047 CATGCTGCTGCTCATCTCTTTTGGCTTCTCCATTTGCTGGCTCAAGCCCTTTGCCGAGAT 1106
Db 253 GATTCCTCTCTTACTTTTTTTGGCTTTTGGCACTGCTGGCTCAATGCCCTTGGTCAGAT 312
QY 1107 GCTACGATTTGAGACAGAGATGTTTACCGGACTGGTGGAACTCAACGCTCTTCTCCAA 1166
Db 313 GTTACGCTTTGGTGACAGATGTTCTATAAGGATTTGGTGAACCTCCACGCTATATCCAA 372
QY 1167 CTACTACCCCACTTGAAGCTGGTCCCTGCTGCTACAGTCTGCTATCATCAGCA 1226
Db 373 CTATTATAGAACCCTGGAATGTGGTGGTCCATGACTGCTATATTACTATGCTTACAAGGA 432

QY 1227 TGGGCTGGGCTCTTGGTGGCCCGAGGGGTAGCCATGCTGGGTGTCTCTGCT 1286
Db 433 CTTTCTCTGGTTTTCTCCACAGAGATTCAAAATCTGCTGCCATGTTAGCTGTCTTTGCTCT 492
QY 1287 CTCGCCAGTGGCCCATGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATATCCCGTCAT 1346
Db 493 ATCTGCTGTAGTACAGATATATGCTTGGCTGTCTTCTGCTTGGAGCTTTTCTATATCCCGTCT 552
QY 1347 GCTGATATCTCTCTTCTGTCATTGGAGGAATGTTGAACCTCATGATCATGACGACG-GCA 1405
Db 553 CTTCGCTCTCTCATGTTCTTTTGGATGCGCTTCAACTTCATGTCATGATAGTCGGA 612
QY 1406 CGGCCCGCATGAGCACTGTCATGTGACCATGCTGTTCTAGGCCAGGAATCCAGG 1465
Db 613 AAAGCCGATCTGGAATGTTCTGATGCTGACTTCTCTTCTTGGCAATGGAGTCTTAC 672
QY 1466 TCAGCTCTGTCGCCAGGAGTGGT 1489
Db 673 TCCTGCTTTTATTCTCTCCAGGAGT 696

RESULT 13
AA867128
LOCUS
DEFINITION
vx23f10.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
(IMAGE:1265323 5' similar to gb:L21934 STEROL O-ACYLTRANSFERASE
(HUMAN); gb:L42293 Mus musculus acyl-coenzyme A:cholesterol
acyltransferase (MOUSE));, mRNA sequence.

ACCESSION
AA867128
VERSION
AA867128.1 GI:2962573
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 887)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilsson,R. and
Waterston,R.

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:667875
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 447.
Location/Qualifiers
1. 887

FEATURES

Source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1265323"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCCGCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:15:41 ; Search time 2498 Seconds
(without alignments)
15792.059 Million cell updates/sec

41
Title: US-09-918-026A-3

Perfect score: 1569

Sequence: 1 atggagcaggcggggcccgcg.....cttggtctgcacacctag 1569

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1569	100.0	1569	1	PCT-US02-22746-3
2	1569	100.0	1569	34	US-09-918-026A-3
3	1564.2	99.7	2040	24	US-09-630-892-4
4	1564.2	99.7	2040	24	US-09-630-892A-4
5	1425.8	90.9	1509	17	US-09-328-857A-2
6	1113.4	71.0	1607	80	US-60-360-207-5649
7	1112.4	70.9	1607	1	PCT-US02-22746-10
8	1112.4	70.9	1607	17	US-09-328-857A-1
9	1112.4	70.9	1607	34	US-09-918-026A-10
10	544.8	34.7	2154	66	US-60-229-512-505
11	421.4	26.9	2924	80	US-60-360-207-10898
12	407.2	26.0	4011	1	PCT-US02-18947-388
13	407.2	26.0	4011	41	US-10-172-118-388
14	405.6	25.9	2022	30	US-09-770-173-2800
15	405.6	25.9	2129	1	PCT-US02-21664-109
16	405.6	25.9	2729	41	US-10-191-997-109
17	405.6	25.9	3499	18	US-09-474-436-6552
18	405.6	25.9	3649	10	US-08-657-621A-1
19	405.6	25.9	3688	23	US-09-606-776-4846
20	405.6	25.9	3688	25	US-09-644-873-10353
21	405.6	25.9	3688	25	US-09-652-126-9964

Qy	Db	Seq ID	Score	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378</
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QY 1321 GTCTGGGGTTCTTCTATCCCGTCATGCTGATCTCTCTTGTCTATGGAGAAATGTTG 1380
Db 1321 GTCTGGGGTTCTTCTATCCCGTCATGCTGATCTCTCTTGTCTATGGAGAAATGTTG 1380
QY 1381 AACTTCATGATCATGACAGCCAGCCGCGGCGCATGGAACGTGCTGATGTGGACCATG 1440
Db 1381 AACTTCATGATCATGACAGCCAGCCGCGGCGCATGGAACGTGCTGATGTGGACCATG 1440
QY 1441 CTGTTTCTAGGCGAGGAATCCAGGTCAGCTGTACTGCCAGGAGTGGTACGACGCGG 1500
Db 1441 CTGTTTCTAGGCGAGGAATCCAGGTCAGCTGTACTGCCAGGAGTGGTACGACGCGG 1500
QY 1501 CACTGCCCTTACCCAGGCAACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTGCG 1560
Db 1501 CACTGCCCTTACCCAGGCAACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTGCG 1560
QY 1561 CATACCTAG 1569
Db 1561 CATACCTAG 1569

RESULT 2

US-09-918-026a-3

; Sequence 3, Application US/0918026A

; GENERAL INFORMATION:

; APPLICANT: Rosanne M. Crooke

; APPLICANT: Mark J. Graham

; APPLICANT: Kristina M. Lemonidis

; TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL ACYLTRANSFERASE-2 EX

; FILE REFERENCE: ISPH-0588

; CURRENT APPLICATION NUMBER: US/09/918,026A

; CURRENT FILING DATE: 2001-07-30

; NUMBER OF SEQ ID NOS: 65

; SEQ ID NO 3

; LENGTH: 1569

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1569)

US-09-918-026a-3

Query Match 100.0%; Score 1569; DB 34; Length 1569;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCCAGGGGGCCGCTGCTGCTGCTGCAGAGCAGAGAGGGCTGGAGGGAGCGG 60

Db 1 ATGGAGCCAGGGGGCCGCTGCTGCTGCTGCAGAGCAGAGAGGGCTGGAGGGAGCGG 60

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QY 121 TGGACCCGACATGAGAGCTGTGAAGGCACAATTGCTGGAGCAAGCGAGGACAACTG 180

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Db 361 CGCACCATCTACCACATGTTTCATCGCTGGCTGTGTCTTTCATCATCAGCACCCCTGGCC 420

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Db 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480
QY 481 GGACAGCTGCCATTTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCTGTGGGG 540
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Db 541 CGGTACACGCGCTTACGCGCTGTGGGCCAGGGCACCTGGACGAGCGGAGGCGCTGGGC 600
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Db 781 GAGGGGATCCAGGCCCGCCAGTTTCTCCAGCTACCTCTACTTCTCTTCTGCCCCAACACTC 840
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Db 841 ATCTACAGGAGACTTACCTTAGGAGCCCTATGTGAGGTGGAAATATGTGGCCAAAGAAC 900
QY 901 TTTGGCCAGCGCTGGGATGTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 TTTGGCCAGCGCTGGGATGTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 CCTGTCTTTGCCAACATGAGCCGAGAGCCCTTTCAGCACCCCGTGCCTGCTCTCTATC 1020
Db 961 CCTGTCTTTGCCAACATGAGCCGAGAGCCCTTTCAGCACCCCGTGCCTGCTCTCTATC 1020
QY 1021 CTGCATGCGACGTTGCCAGGATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 CTGCATGCGACGTTGCCAGGATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
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Db 1141 TGTGGAACCTCAACGCTCTTCTCCAACTACTACCGCACTTGGAACTGGTGGTCCATGAC 1200
QY 1201 TGGCTGTACAGCTACGCTGTATCAGGATGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 TGGCTGTACAGCTACGCTGTATCAGGATGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1260
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Db 1261 GTAGCCATGCTGGGTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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Db 1321 GTCTGGGGTTCTTCTATCCCGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
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Db 1381 AACTTCATGATGATGACAGCCAGCCGCGGCGCATGGAACGTGCTGATGTGGACCATG 1440
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Db 1441 CTGTTTCTAGGCGAGGAATCCAGGTCAGCTGTACTGCCAGGAGTGGTACGACGCGG 1500

Qy 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGGTGACACCTCGATCTTGCTCTGC 1560
Db 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGGTGACACCTCGATCTTGCTCTGC 1560
Qy 1561 CATACCTAG 1569
Db 1561 CATACCTAG 1569

RESULT 3
US-09-630-892-4
; Sequence 4, Application US/09630892
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331-A
; CURRENT APPLICATION NUMBER: US/09/630.892
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Yeast
US-09-630-892-4

Query Match 99.7%; Score 1564.2; DB 24; Length 2040;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGCCAGGCGGCGCTGCTGCTGCTGAGAGGACAGAGGCTGGAGGGAGCGG 60
; Db 52 ATGGAGCCAGGCGGCGCTGCTGCTGCTGAGAGGACAGAGGCTGGAGGGAGCGG 111
Qy 61 GAGCGCCAAACCCTGTGGAGATGGAACACTGAGACGACAGAGCCCCGGACTTGTGTACAA 120
; Db 112 GAGCGCCAAACCCTGTGGAGATGGAACACTGAGACGACAGAGCCCCGGACTTGTGTACAA 171
Qy 121 TGGACCCGACACATGGAGCTGTGAAGCACAATGCTGGAGCAGCAGCGACCAACTG 180
; Db 172 TGGACCCGACACATGGAGCTGTGAAGCACAATGCTGGAGCAGCAGCGACCAACTG 231
Qy 181 AGGAGCTGCTGGATCGGCGCCATGGGGAGGCTATACATCTCCATCCCAACAGACAAA 240
; Db 232 AGGAGCTGCTGGATCGGCGCCATGGGGAGGCTATACATCTCCATCCCAACAGACAAA 291
Qy 241 CTTCTGCCCCACCTCCCGAGGTTCTTGGAGCAGGACCCAGGAGCCATCCCTGGGGAAA 300
; Db 292 CTTCTGCCCCACCTCCCGAGGTTCTTGGAGCAGGACCCAGGAGCCATCCCTGGGGAAA 351
Qy 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTATGAGCTGATGGAGTGCAGCATTTTC 360
; Db 352 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTATGAGCTGATGGAGTGCAGCATTTTC 411
Qy 361 CGCACCATCTTACACATGTTTCATCGCTGCGCTGTGTCTTTCATCATGACACCCCTGGCC 420
; Db 412 CGCACCATCTTACACATGTTTCATCGCTGCGCTGTGTCTTTCATCATGACACCCCTGGCC 471
Qy 421 ATGACTTTCATGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTTC 480
; Db 472 ATGACTTTCATGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTTC 531
Qy 481 GGACAGCTGCATTGGCGCTGTGTGACTGGTGGCCCATGTTTCTGCCACCCCTGTGGCG 540
; Db 532 GGACAGCTGCATTGGCGCTGTGTGACTGGTGGCCCATGTTTCTGCCACCCCTGTGGCG 591
Qy 541 CCCTACAGGCCCTTACGGCTGTGGGCGAGGGGACCTTGACGCGAGCGAGCGGCGCTGGGC 600
; Db 592 CCCTACAGGCCCTTACGGCTGTGGGCGAGGGGACCTTGACGCGAGCGAGCGGCGCTGGGC 651
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RESULT 4
US-09-630-892A-4
; Sequence 4, Application US/09630892A
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.

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Qy 661 GAGCATACGCTCCCGCGGCTCCCGTGTGTGCTGCTTCCAGCAGGTTAGTGTCTG 720
Db 712 GAGCATACGCTCCCGCGGCTCCCGTGTGTGCTGCTTCCAGCAGGTTAGTGTCTG 771
Qy 721 ATGAAAGCTACTCTTCTGAGAGAGGCTGTGCTGGGATCCTTCTGCGCAGAGAGGT 780
Db 772 ATGAAAGCTACTCTTCTGAGAGAGGCTGTGCTGGGATCCTTCTGCGCAGAGAGGT 831
Qy 781 GAGGGATCCAGGCGCCGAGTTTCTCCAGTACCTTCTCTCTCTCTCTCTCTCTCTCT 840
Db 832 GAGGGATCCAGGCGCCGAGTTTCTCCAGTACCTTCTCTCTCTCTCTCTCTCTCTCT 891
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Db 892 ATCTACAGGAGACTTACCTTAGGAGCGCTATGTGAGTGAATATATGCGCCAGAAC 951
Qy 901 TTTGCCAGGCGCTGGGATGTGTGCTGTATGCTGCTTCTCTCTCTCTCTCTCTCTCT 960
Db 952 TTTGCCAGGCGCTGGGATGTGTGCTGTATGCTGCTTCTCTCTCTCTCTCTCTCTCT 1011
Qy 961 CTTGTCTTTGCCAACATGAGCGGAGAGCGCTTCCAGCACCGTCCCTGGTGTCTCTATC 1020
Db 1012 CTTGTCTTTGCCAACATGAGCGGAGAGCGCTTCCAGCACCGTCCCTGGTGTCTCTATC 1071
Qy 1021 CTGCATGCCACGTTGCCAGGATCTTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1072 CTGCATGCCACGTTGCCAGGATCTTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1131
Qy 1081 TGCTGGCTCAAGCGCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1140
Db 1132 TGCTGGCTCAAGCGCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1191
Qy 1141 TGTGGAACTCAAGCTCTTCTCCAACTACTACCGACTTTGGAACCTGTGTCTCTATGAC 1200
Db 1192 TGTGGAACTCAAGCTCTTCTCCAACTACTACCGACTTTGGAACCTGTGTCTCTATGAC 1251
Qy 1201 TGGCTGTACAGCTACGTTATCAGGATGGGCTGCGGCTCTCTGCTGCTCTCTCTCTCT 1260
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Db 1312 GTAGCCATGCTGGGTGTTCTCTGCTGCTCGCAGTGGCCCATGAGTATATCTTCTGCTTC 1371
Qy 1321 GTCCTGGGGTTCTTCTATCCCGTCATCTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1372 GTCCTGGGGTTCTTCTATCCCGTCATCTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1431
Qy 1381 AACTTCATGATGATGACCGAGCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1440
Db 1432 AACTTCATGATGATGACCGAGCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1491
Qy 1441 CTGTTTCTAGCGCAGGGAATCCAGGCTGAGCTGTACTGCCAGGAGTGTATCGCAGCGCG 1500
Db 1492 CTGTTTCTAGCGCAGGGAATCCAGGCTGAGCTGTACTGCCAGGAGTGTATCGCAGCGCG 1551
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Qy 1561 CATACCTAG 1569
Db 1612 CATACCTAG 1620


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; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; FILE REFERENCE: 0575/56331-A
; CURRENT APPLICATION NUMBER: US/09/630,892A
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Yeast
US-09-630-892A-4

Query Match      99.7%: Score 1564.2; DB 24; Length 2040;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGAGCCAGGCGGGCCCGTCTGCGTCTGACAGAGGACAGAGGCTGGAGGGAGCGG 60
DB 52 ATGGAGCCAGGCGGGCCCGTCTGCGTCTGACAGAGGACAGAGGCTGGAGGGAGCGG 111
QY 61 GAGCGCCAAACCTGTGGAGATGGAACACTGAGAGCCACAGAGCCCGGACTTGGTACAA 120
DB 112 GAGCGCCAAACCTGTGGAGATGGAACACTGAGAGCCACAGAGCCCGGACTTGGTACAA 171
QY 121 TGGACCCGACACATGAGGCTGTGAAGCACAATTTGCTGGAGCAAGCGCAGGACAACCTG 180
DB 172 TGGACCCGACACATGAGGCTGTGAAGCACAATTTGCTGGAGCAAGCGCAGGACAACCTG 231
QY 181 AGGAGCTGCTGGATCGGGCCATGCGGAGGCTATACAACTTACCATCACAAGACAAA 240
DB 232 AGGAGCTGCTGGATCGGGCCATGCGGAGGCTATACAACTTACCATCACAAGACAAA 291
QY 241 CTTCTGCCCCACCTCCCGGAGTTCTTGACAGAGCCAGGAGCCATCCCTGGGGAAA 300
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DB 412 CGCACCATCTACCATGTTTCACTGCTGCGCTGTGTGCTTTCATCATCAGCACCCTGGCC 471
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QY 481 GGACAGCTGCCATTTGGCGTGGTGACCTGGGTGGCCATGTTTCTGTCCACCCCTGTTGGG 540
DB 532 GGACAGCTGCCATTTGGCGTGGTGACCTGGGTGGCCATGTTTCTGTCCACCCCTGTTGGG 591
QY 541 CCGTACCGAGCCCTAGGCGTGGGCGAGGCGACCTGGACCGAGCGGCGGCTGGCG 600
DB 592 CCGTACCGAGCCCTAGGCGTGGGCGAGGCGACCTGGACCGAGCGGCGGCTGGCG 651
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DB 652 TGTGCGCTTTTAGCGCGCCACCGCTGTGTGCTGTGCGCGCTCGCGGTCCACGTGGCCGTG 711
QY 661 GAGCATCAGCTCCCGCGGCTCCCGCTGTGTGCTGTGCTTTCAGCAGGTTAGGTTCCGTG 720
DB 712 GAGCATCAGCTCCCGCGGCTCCCGCTGTGTGCTGTGCTTTCAGCAGGTTAGGTTCCGTG 771
QY 721 ATGAAAGCTACTCTCTCTGAGAGGCTGTGCTGGATCTTCGTCAGCAGGTTAGGTTCCGTG 780
DB 772 ATGAAAGCTACTCTCTCTGAGAGGCTGTGCTGGATCTTCGTCGACAGGCTTCGTCGACAGG 831
QY 781 GAGGGATCCAGGCGCCCGGCTTCTCCAGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
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DB 892 ATCTACAGGAGACTTACCCTAGGAGCGCCTATGTCAGGTGGAATTTATGTGGCCAAGAAC 951
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DB 952 TTTGCCAGGCGCTGGGATGTGTCTATGCTGCTTCTCATCTGCGGCGCCTCTGTGT 1011
QY 961 CTTGTCTTTGCCAACATGAGCGGAGAGCGCCTTCAGCACCGGTCGCTGCTCTATC 1020
DB 1012 CTTGTCTTTGCCAACATGAGCGGAGAGCGCCTTCAGCACCGGTCGCTGCTCTATC 1071
QY 1021 CTGCATGCCACCTTCCAGGCACTTCATGCTGCTGCTCATCTTCTTTGCCCTTCCCTCAT 1080
DB 1072 CTGCATGCCACCTTCCAGGCACTTCATGCTGCTGCTCATCTTCTTTGCCCTTCCCTCAT 1131
QY 1081 TCCTGGCTCAACGCTTTCCGAGATGCTACGATTTGGAGAGAGGATGTTCTACCGGGAC 1140
DB 1132 TCCTGGCTCAACGCTTTCCGAGATGCTACGATTTGGAGAGAGGATGTTCTACCGGGAC 1191
QY 1141 TGGTGGAACTCAACGCTTCTTCCAACTACTACCGCACTTGGAACTGCTGCTTCCATGAC 1200
DB 1192 TGGTGGAACTCAACGCTTCTTCCAACTACTACCGCACTTGGAACTGCTGCTTCCATGAC 1251
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QY 1321 GTCTGGGCTTCTTCTATCCGCTCATGCTGATCTTCTTGTCTATTTGGAGGAATGTTG 1380
DB 1372 GTCTGGGCTTCTTCTATCCGCTCATGCTGATCTTCTTGTCTATTTGGAGGAATGTTG 1431
QY 1381 AACTTCATGATCATGACAGCGACCGCGCGGCACTGGAACGTGCTGATGTGGACCATG 1440
DB 1432 AACTTCATGATCATGACAGCGACCGCGCGGCACTGGAACGTGCTGATGTGGACCATG 1491
QY 1441 CTGTTTCTAGGCGAGGAAATCCAGGTCAGCTGACTGTCAGGAGTGTGACGACGCGG 1500
DB 1492 CTGTTTCTAGGCGAGGAAATCCAGGTCAGCTGACTGTCAGGAGTGTGACGACGCGG 1551
QY 1501 CACTGCGCTTACCAGGCAACTTCTTGGGGCTGCTGACACCTGCTGCTGCTGCTGCTG 1560
DB 1552 CACTGCGCTTACCAGGCAACTTCTTGGGGCTGCTGACACCTGCTGCTGCTGCTGCTG 1611
QY 1561 CATACCTAG 1569
DB 1612 CATACCTAG 1620
```

```
RESULT 5
US-09-328-857A-2
; Sequence 2, Application US/09328857A
; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; APPLICANT: Farese, Robert
; APPLICANT: Novak, Sabine
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Novel Acyl CoA:Cholesterol Acyl
; FILE REFERENCE: 6510-104US1
; CURRENT APPLICATION NUMBER: US/09/328,857A
; CURRENT FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/090,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1509
```


171	Db	171	AAGACNCGATTTCTGGAGCAAGCACAGAGAGTTGGCAGAGCTGTGGATCGGGCCCTA	230
205	Qy	205	CGGAGGCTATACAATCCTACCCATCACAAAGAAACCTCTGCCCCACCTCCOCCCAAGGT	264
231	Db	231	JGGAGGCTATGCAAGCTTACCCCAAACAAGACAGACCTCTTCCCTCCGCTGCCCCAGAT	290
265	Qy	265	TCCTTGGACAGGACCCAGAGGCCATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAG	324
291	Db	291	TCTACAAGCAGACCCCGGAGTTACGCCCTTGAAACGGAAAGTTTTCGTGCGCCGCAAG	350
325	Qy	325	TCCCTGCTTGATGAGCTGATGGAGGTGCAGACTTTCGGCACCACATCTACCACATGTTTCATC	384
351	Db	351	TCATGATGATGAGCTAATGGAGGTGCACACTTCGGAACCATCTACCACATGTTTCATA	410
385	Qy	385	GCTGGCCTGTGTCTTCATCATCAGACCCCTGGCCATCGACTTCATTTGATGAGGGCAGG	444
411	Db	411	CGGGCCCTATGGTTCTTTGATCATCAGACCCCTGGCCATCGACTTCATTTGATGAGGGCAGG	470
445	Qy	445	CTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGTG	504
471	Db	471	TGATGCTGGAGTTTGACTTACTCTCTTCAGCTTCGGACAGCTGCCCTTGGCGCTGATG	530
505	Qy	505	ACCTGGGTGCCATGTTTCTGTCCACCTGTTGGCCCGCTACAGGCCCTACGGCTGTGG	564
531	Db	531	ACCTGGGTTCACATGTTCTCTGTATAGCTCCTAGTCCCTACAGACCCCTGGCTGTGG	590
565	Qy	565	GCCA-----GGGCACCTGCAGCCAGCCAGCGGCTGGCGCTGGCGCTTTTA	612
591	Db	591	GCCAGGCCGCGGTGGGGTGCCGTGATGCTGGGGCCAGCCTGGGCTGCTTCTGCTG	650
613	Qy	613	GCGGCCACGCGTGTGTCTCTGCGCGCTCCCGGTCCAGCTGGCCGTGGAGCATCAGTCT	672
651	Db	651	GCTGCCACGCTGTGTGCTCTGCTGCTCCCGTGCAGCTGCAGTGACGAGCATGAGCTT	710
673	Qy	673	CGCGCGGCTCTCCGTTGTGCTCGTCTTCGACGAGTTAGTTCTCTGATGAAAGCTAC	732
711	Db	711	CGCGCGGCTCGCGCTCGCTCTTTGACGAGGTAGATGCTGATGAAAGCTAC	770
733	Qy	733	TCTTCTCTGAGAGGCTGTGCCCTGGATCCTTCGTGCCACAGAGGTGAGGGGATCCAG	792
771	Db	771	TCTTCTCTGAGAGACTGTGCCTGGATCTTTGTGTCAGAGAGGAAAGGCATCAGC	830
793	Qy	793	GCCCCAGTTTCTCAGTCACTACTCTCTCTGCCCCACACATCATCTACAGGAG	852
831	Db	831	CCCCCAAGTTTCTCAGTCACTACTCTCTCTGCCCCACACATCATCTACAGAG	890
853	Qy	853	ACTTACCCTPAGACGCCCTATGTCAAGTGGAAATATATGGCCAAAGAACTTTGCCAGGCC	912
891	Db	891	ACATACCCAGACACCCAGCATCAGGTGGAATATGTGGCAGAAGAACTTTGCCAGGTC	950
913	Qy	913	CTGGGATGTGCTCTATGCGCTTCATCTCGGCGCGCTCTGTGTTCTGCTCTTGCC	972
951	Db	951	CTGGGCTGTTGCTCTATGCTCTTCACTCCTGCGCGCGCTCTGTGCTCTGCTTGCC	1010
973	Qy	973	AACATAGCCGAGAGCCCTTCAGCACCGCTGCTGCTGCTCTCTATCTCTGCATGCCACG	1032
1011	Db	1011	ARCATAGCCGGGAACCCCTTCAGCACCCGGGCTCTGCTCTCCATCTTGCATGCCACG	1070
1033	Qy	1033	TGCCAGGCATCTTCATGCTGCTCATCTCTTTGCCCTTCCTCCATGCTGGCTCAAC	1092
1071	Db	1071	GGGCCAGGCATCTTCATGCTGCTCCTCATCTTCTCGCCTTCCTGCACTGCTGGCTCAAC	1130
1093	Qy	1093	GCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGAACCTCA	1152
1131	Db	1131	GCCTTTGCCGAGATGCTGCGGTTTGGAGACAGGATGTTCTACCGGGACTGGTGAACCTCG	1190
1153	Qy	1153	ACGTCTCTCCAACTACTACCGCACTTGGAAACGTGTGGTCCATGACTGGCTGTACAGC	1212
1191	Db	1191	ACTTCTCTTCCAACTACTACCGCACTTGGAAACGTGTGGTCCATGACTGGCTGTACAGC	1250
1213	Qy	1213	TACGTGTATCAGGATGGGCTGGGCTCTTTGGTGGCCCGGCGGAGACCATGCTG	1272
1251	Db	1251	TATGTTATCAAGATGGGCTGGCTCTTTAGCAGCGGGGCTGCGGGGTTCCATGCTG	1310

QY	1273	GGTGTGTTCTCGTCTCCGACGTGGCCCATAGTATATCTTCTGCTCGCTGGGGTTC	1333
Db	1311	GGAGTGTTCTCGTGTCTCGGGTGGTTTCATGAGTATATCTTCTGCTCGCTGGGGTTC	1370
QY	1333	TTCTATCCCGTCATGCTGATACTCTTCTTGTCTGAGGAAATGTTGAACITTCATGATG	1392
Db	1371	TTCTATCCCGTCATGCTGATGCTATTCCTTGTGTTGTTTCGGGGGGCTGCTGAATTTCAACCATG	1430
QY	1393	CATGACACGACGCGCCGGCGCATGGAACGTCGTGATGTGGACCATCTGCTTTCTTAGGC	1452
Db	1431	AACGACAGGACACACAGGTCACGCTGACACATCTTCATGTGGAACCTTCTCTTCATGGGC	1490
QY	1453	CAGGGAATCCAGGTCACGCTGTACTGCCAGGAGTGGTAGCGACGGCGGCACATGCCCTTA	1512
Db	1491	CAGGCAATCCAGGTCACGCTTATCTACTGCCAGGAGTGGTAGCTCGTGACACTGTCCCGCTG	1550
QY	1513	CCCCAGGCACTTCTTGGGGGCTGGTGACACCTCGCATCTTGCTCTGGCATAACCTAG	1569
Db	1551	CCCCAGACACATCTCGGGGATGGTGACACCCCAATCTTGTCTCTGCCATACCTAG	1607

```

RESULT 8
US-09-328-857A-1
; Sequence 1, Application US/09328857A
; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; APPLICANT: Farese, Robert
; APPLICANT: Novak, Sabine
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Novel Acyl CoA:Cholesterol Acyl
; TITLE OF INVENTION: Transferase (ACAT-2)
; FILE REFERENCE: 6510-104US1
; CURRENT APPLICATION NUMBER: US/09/328,857A
; CURRENT FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/090,354
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1607
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (176)...(176)
; OTHER INFORMATION: N means a, g, c or t
US-09-328-857A-1

```

	Query Match	70.9%	Score 1112.4;	DB 17;	Length 1607;
	Best Local Similarity	83.2%;	Pred. No. 1.4e-237;		
	Matches 1295;	Conservative	0;	Mismatches 247;	Indels 15; Gaps
Qy	28	CTCCAGACGACAAGGGCTGGAGGGGAGCGGAGCGGCCAAACCCTGT---	GGAGATGGA	84	
Dd	51	CTTCGGAGGAGAGAAGGCTGGAGAGGAGCAGGAGGAGGAGCCGCTGGAGGAGAAGGG	110		
Qy	85	AACACTTGAGACGCACAGACCCCGGACATTGGTACAAATGGACCCGACACATGGAGGCTGTG	144		
Dd	111	AACGCCAAGGACACACGGAACCCGACACTTGGTGTCAATTTGGACTCGACATATGGAGGCTGTG	170		
Qy	145	AAGSGCAATTTGTGGAGCAAGCGCAGGGACAACCTGAGGGAGCTGTCTGGATCGSGGGCCATG	204		
Dd	171	AACACNCAGTTTCTGGAGCAACACACAGAGAGATTGGCAGAGACTGTTGGATCGSGGCCCTA	230		
Qy	205	CGSGAGGCTATACAATCTTACCCTATCACAGACAACCTCTGCCCCCACCTCCCCCAGGT	264		
Dd	231	TGGGAGGCTATGCAAGCTTTACCCCAAACAGACAGACCTCTTCCCTTCGCTGCCCCACAGAT	290		
Qy	265	TCCTTGAGCAGGACCCAGGAGGCATCCCTCTGGGGAACAGAAAGTTTTTCATCATCCGCAAG	324		
Dd	291	TCTATACAGCAGACCCCGAGTTAGSCCTCTGAAAACCGAAAGTTTTTCGTGCCGCCGCAAG	350		

Db 531 ACCTGGTCCCATGTTCTCTGTATACGCTCTAGTCCCTACAGACCTCTGTGGCTGG 590
Qy 565 GCCA-----GGGSCACCTGGACGACGACGGGCTGGGCTGTGGCTTTTA 612
Db 591 GCCAGCGCGCGCTGGGGTCTGTGATGCTGGGGCCAGCGTGGCTGCTTCTGCTG 650
Qy 613 GCGGCCACCGCTGTGCTGCGGCTGCGGCTCAGCTGCGGCTGGAGCTAGCTC 672
Db 651 GCTGCCACGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
Qy 673 CCGCGGCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db 711 CCGCGGCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Qy 733 TCCCTCTGAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
Db 771 TCCCTCTGAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
Qy 793 GCGCGGCTCTCCAGCTACCTCTCTCTCTCTGCGCCAACTCATCTACAGGAG 852
Db 831 CCGCGGCTCTCCAGCTACCTCTCTCTCTCTGCGCCAACTCATCTACAGGAG 890
Qy 853 ACTTACCTTAGGAGCGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912
Db 891 ACATACCGCCAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 950
Qy 913 CTGGAGTGTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
Db 951 CTGGGCTGTTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010
Qy 973 AACATGACCGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
Db 1011 AACATGACCGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
Qy 1033 TTGCCAGGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Db 1071 GGGCCAGGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
Qy 1093 GCTTTGCGGAGATGCTACGATTTGGACAGGATGTTTACCGGGAGCTGGTGAAC 1152
Db 1131 GCTTTGCGGAGATGCTGGGTTTGGACAGGATGTTTACCGGGAGCTGGTGAAC 1190
Qy 1153 AGCTCTCTTCCAACTACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
Db 1191 ACTTCTCTTCCAACTACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1250
Qy 1213 TAGCTGATACGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
Db 1251 TAGTGTATCAAGATGGCTGTGGCTCTTAGCGAGCGGGCTCGGGGTGGCCATGCT 1310
Qy 1273 GGTGTGTTCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1332
Db 1311 GGAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
Qy 1333 TTCTATCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1392
Db 1371 TTCTATCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1430
Qy 1393 CATGACCGGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
Db 1431 AAGCAGGACACAGGCTCCAGCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 1490
Qy 1453 CAGGGAATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
Db 1491 CAGGCAATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1550
Qy 1513 CCGCAGGCACTTTCTGGGGCTGGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1569
Db 1551 CCGCAGGCACTTTCTGGGGCTGGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1607

US-60-229-512-505
; Sequence 505, Application US/60229512
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHASE II
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000770
; CURRENT APPLICATION NUMBER: US/60/229,512
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 505
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-512-505

Query Match 34.7%; Score 544.8; DB 66; Length 2154;
Best Local Similarity 65.8%; Pred. No. 6.3e-111;
Matches 878; Conservative 0; Mismatches 357; Indels 99; Gaps 2;
Qy 189 GCTGGATCGGCGCATCGGGAGGCTATACATCTTACCCATCACAGACAAACCTCTG 248
Db 541 GCTGGATCGGCGCATCGGGAGGCTATACATCTTACCCATCACAGACAAACCTCTG 600
Qy 249 CCCACCTCCCGAGGTTCTTGAGCAGGACCCAGAGCCATCCCTGGGGAACAAAGT 308
Db 601 CCCACCTCCCGAGGTTCTTGAGCAGGAGTCTGGGGAATGGGTGCGGGGCTCTCT 560
Qy 309 TTTTCATCTCCGCAAGTCTGCTGATGAGCTGATGAGGTGAGGAGTTCGACACCT 368
Db 661 GTAGCAGATCATGAGCCCTGCTGAGTANGTTCGGGGTATGACAAGTAATGGAG 720
Qy 369 CTACCATGTTTCATCGCTGGCTGTGTCTTCATCATCAGCACCTGGCCATCGACT 428
Db 721 AAGAAAGGGCTTTGGCTCTGGCTGTGTCTTCATCATCAGCACCTGGCCATCGACT 780
Qy 429 CATGTAGTGGGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGACAG 488
Db 781 CATGTAGTGGGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGACAG 840
Qy 489 GCCATTGGCGCTGGTACCTGGTGGTGGCCATGTTTCTGTCCACCTGTTGGCGCGTAC 548
Db 841 CCCTCTGGCGCTGGTACCTGGTGGTGGCCATGTTTCTGTCCACCTGTTGGCGCGTAC 900
Qy 549 GGCCCTAGGCTGTGGCCAGGCGCACCTGGACGAGGCGGCTGGGCTGTGCGCT 608
Db 901 GGCCCTAGGCTGTGGCCAGGCGCACCTGGACGAGGCGGCTGGGCTGTGCGCT 960
Qy 609 TTTAGCGCGCCACCGCTGCTGCTGCGCTGCGGCTCCAGTGGCGCTGGAGCATCA 668
Db 961 GCTAGCGCGCCACCGCTGCTGCTGCGCTGCGGCTCCAGTGGCGCTGGAGCATCA 1020
Qy 669 GCTCCCGCGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
Db 1021 GCTCCCGCGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 729 CTACTCTCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db 1081 ACGGACAGGAAGAACCCAGTGGTGGGCGGATCTTCTGCTGCTGCTGCTGCTGCTGCT 1140
Qy 789 CCAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
Db 1141 CATCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Qy 849 GGAGACTTACCTAGGAGCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
Db 1201 GGAGACTTACCTAGGAGCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Qy 909 GGCCCTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968
Db 1261 ACTTAGAAGATAGGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

Query Match 26.0%; Score 407.2; DB 41; Length 4011;
Best Local Similarity 59.0%; Pred. No. 3.6e-80;
Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;

QY 287 CATCCCTCGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGG 346
DB 1737 CACCTCCAGAACAGAAAGATTTTATTTGCAAGCGCTCTCTCTAGATGAAGCTGTG 1796

QY 347 AGGTGACGATTTCCGACCATCTACCATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406
DB 1797 AAGTGGACACATCAGAACATATATCATGTTTATTTGCCCCCTCTCATCTCTTTATACC 1856

QY 407 TCAGCACCTCGGCCATCGACTTCATTTGATGAGGAGGCTGCTGCTGGAGTTTGACCTAC 466
DB 1857 TCAGCACACTTCTAGTAGATACATTTGATGAAGAGGCTGCTGCTGAGTTTCAGCCTCC 1916

QY 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGGTGACCTGGGTGGCCATGTTTCGT 526
DB 1917 TGCTTATGCTTTTGGCAAAATTTCTACCGTTTGTGGACCTGGTGGATCATGTTCTCTGT 1976

QY 527 CCACCTGTTGGCGCTACAGGCCCTAGGCTGTGGGCCAGGGGCACTTGACGACGAGG 586
DB 1977 CTACATTTTCAGTCCCTATTTTCCTGTTTCAACATTTGGCCACTGGCTATACGAAGTT 2036

QY 587 CGACGGGCTGGGCTGTGCGCTTTTAGCGCCCGCCAGCGCTGGTGTCTGCGCGCTGCCGG 646
DB 2037 CTCATCCGCTGATCGTCTCTCTCTCCATGGCTTTCTTCATGATCTTCCAGATGGAG 2096

QY 647 TCC-----ACGTGGCGTGGAGCATCAGCTCCCGCGGCTCCCGTT 688
DB 2097 TTCTAGGTTTGGACCAACATATATGTTGTAGCATATACACTGCCACGACTCCCGGT 2156

QY 689 GTGCTCGTCTTCAGCAGGTTAGTTCCTCATGAAAGCTACTCCTCTCCCTGAGAGG 748
DB 2157 TCATCATATATTCAGCAGATTCGTTTGTATGAAGGCCCACTCATTTGTCAGAGAGA 2216

QY 749 CTGTCCTGGGATCCTTCGTGCCAGCAGGTGAGGGATCCAGGCCCGCCAGTTCTTCCA 808
DB 2217 AGTGCTCGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACGTGTTCCAAATACCTACA 2275

QY 809 G-----CTACCTACTCTCTCTCTGCCCCAACACATCATCTACAGGAGACTTACCT 861
DB 2276 GTCAACAGATTTTGTACTCTTATTTGCTCTACCTCTATATACCGTGACAGCTATCC 2335

QY 862 AGGAGCCCTATGTCAGGTGGAATATATGGCCAAAGACTTTGCCAGGCCCTGGGATGT 921
DB 2336 AGGAATCCCACTGTAAAGTGGGTTATGTCGTATGAAGTTTGCACAGCTTTTGGTTGC 2395

QY 922 GTGCTATATGCTGCTTCATCTCGGCGGCTCTGTGTTCTGCTCTTTGCCCCAATGAGC 981
DB 2396 TTTTCTATGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTTGTTCCGAATATCAA 2455

QY 982 CGAGAGCCCTTCAGCACCCTGCTGCTGCTCTATCTATCTCCATGCCACGTTGCCAGC 1041
DB 2456 CAGGAGCCCTTCAGGCTGCTGCTTCTGCTCTATGTTATTAACCTCACTTGGCAGGT 2515

QY 1042 ATCTTCATGCTGCTGCTCATCTCTCTGCTTCTCTCCATTTGCTGCTCAACGCTTTGCC 1101
DB 2516 GTGCTGATCTCTCTTACTTTTGTGCTTTTGTGCTGCTGCTCAATGCCCTTGT 2575

QY 1102 GAGATGCTACGATTTGGAGACGATGTTTACCAGGATGTTGGAACATCAACGCTCTTC 1161
DB 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGGAACCTCCACGTCATAC 2635

QY 1162 TCCAACTACTACCGCACTTGGAACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
DB 2636 TCCAACTATATAGAACCTGGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2695

QY 1222 CAGGATGGGCTCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281
DB 2696 AAGGACTTCTCTGCTTTTCTCCAAAGAGATTCAAATCTGCTGCTGCTGCTGCTGCTT 2755

QY 1282 CTGGTCTCGCAGTGGCCCATGAGTATATCTTCTGCTCTCGGGTCTTCTTATCC 1341
DB 2756 GCTGTATCTGCTGTAGTACACCAATATGCTTGGCTGTTGCTTGGCTTCTTATCC 2815

QY 1342 GTCATGCTGATACTCTTCTTGTTCATTTGAGGAATGTTGAACCTTCATGATGATGAC 1401
DB 2816 GTGCTCTGCTCTCTCTTCTTGTGAATGGCTTTCAACTTCTATGTCATGATAGT 2875

QY 1402 CGACCCGCGCCGCACTGGAACCTGCTGATGTGACCATCTGTTCTAGCCAGGAATC 1461
DB 2876 CGAAAAACCCGATTTGGAATGTTCTGATGTGACTTCTTTCTTGGCAATGAGGTC 2935

QY 1462 CAGGTCAGCTGCTACTGCCAGGAGTGTAGCACGCGGCACTGCCCTTACCCAGGCA 1521
DB 2936 TTACTCTGCTTTTATTTCAAGATGGTATGCACGTGCGCACTGTCTCTGAAATATCC 2995

QY 1522 ACTTTCTGGGCTGCTGACACCTCGATCTTGTCTGCTGCCAT 1563
DB 2996 ACATTTTGGATTATGTCGGCCACGTTCTCTGACTTGTCTGT 3037

RESULT 14

US-09-770-173-2800

; Sequence 2800, Application US/09770173

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 1600.2059-001

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,876

; PRIOR FILING DATE: 2000-01-28

; NUMBER OF SEQ ID NOS: 3167

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2800

; LENGTH: 2022

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-770-173-2800

Query Match 25.9%; Score 405.6; DB 30; Length 2022;

Best Local Similarity 58.9%; Pred. No. 7.1e-80;

Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

QY 287 CATCTCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTGATGAGCTCATGG 346
DB 504 CACCTCCAGAACAGGAAAGATTTTATTTGCAAGGCGCTCTCTCTTAGATGAACCTCTTG 563

QY 347 AGGTGACGATTTTCCGCACTCTACCATGTTTCATCGCTGGCCCTGTGTCTTTCATCA 406
DB 564 AAGTGGACCATCATCAGAACATATATCATGTTTATTTGCCCTCTCTCTCTTTATCC 623

QY 407 TCAGCACCTTGGCCATCGACTTCATTTGATGAGGAGGCTGCTGCTGGAGTTTGACCTAC 466
DB 624 TCAGCACACTTGTAGTAGATTACATTTGATGAAGAGGCTGGTGTGATTCAGCTCC 683

QY 467 TCATCTTCAGCTTCGACAGCTGCCATTGCGCTGCTGACCTGGGTGCCCATGTTTCTGT 526
DB 684 TGTCTATGCTTTTGGCAATTTTCTTACCGTTGTTTGGACCTGGTGGATCATGTTCTCTGT 743

QY 527 CCACCTGTTGGCGCGTACCAGGCCCTACGGCTGTGGGCCAGGGCACTTGACACGAGG 586
DB 744 CTACATTTTTCAGTCCCTATTTTCTGTTTCAACATTTGGGCCACTGGCTATACGAAGTT 803

QY 587 CGACGGGCTGGGCTGTGCGCTTTTAGCGCCACGCCGCTGCTGCTGCTGCTGCTGCTGCT 846
DB 804 CTCATCGCTGATCGTCTCTCTCTTCCATGCTGCTTTTTCATGATCTTCTCCAGATTGGAG 863

QY 647 TCC-----ACGTGGCGTGGAGCATCAGCTCCCGCGGCTCCCGTT 688
DB 864 TTCTAGGTTTGGACCAACATATGTTGTTAGCATATACATGGCCACGACTTCCCGGT 923

689 GTGCTCTGGTCTTCAGCAGGTTAGTTCCTGATGAAAGACTACTCTCTCTCTGAGAGG 748
 924 TCATCATTTATATTCAGCAGATTCGTTTGTATGAAGCCCACTCAATTCAGAGAGA 983
 749 CTGTGCTGGGATCTTCGTGCCAGACGAGGTGAGGGATCCAGGCCCAAGTTCTTCCA 808
 984 ACGTGCTCGGTACTAAT-TCAGTAAGGAGAAATCAAGCACTGTTCCTCAATACCTACA 1042
 809 G-----CTACCTCTACTCTCTCTCTGCCCCAACACTCATCTACAGGAGACTTACCT 861
 1043 GTCACCAAGTATTTGTACTCTCTATTTGCTCTACCTTATCTACCGTGACAGCTATCCC 1102
 862 AGSAGCCCTATGTCAGGTGGAATATATGGGCCAAGAACTTTGCCCGCCCTGGGATGT 921
 1103 AGAATCCCACTGTAAGATGGGTTATGTCGCTATGAAGTTTGACAGGCTCTTGGTGTG 1162
 922 GTGCTCTATGCGTCTCATCTGCGCGCCCTCTGTTCTGCTCTCTTGGCCAAATGAGC 981
 1163 TTTTCTATGTGACTACATCTTTGAAGGCTTTGTGCCCTCTGTTTCGGNAATACAA 1222
 982 CGAGAGCCCTTCAGCACCGCTGCCCTGTGTCTCTATCTCTGTCATGCCAGGTGCCAGC 1041
 1223 CAGSAGCCCTTCAGCGCTCGTGTCTGTGCTCTATGTATTTAACTCCATCTGCCAGT 1282
 1042 ATCTTCATGCTGCTCATCTCTTTGCTCTCCCTCCATTTGCTGCTCAAGCCCTTTGCC 1101
 1283 GTGCTGATTCTCTCTTACTTTTTTGGCTTTTGTGACTGCTGGCTCAAGCCCTTGT 1342
 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACGGGAGTGTGGAACCTCAACGCTCTC 1161
 1343 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGGAACCTCCACGCTAC 1402
 1162 TCCAACCTACTACGCACTTGGACGCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
 1403 TCCAACCTATTATAGAACCTGGAATGTTGGTGGTCCATGCTGCTGCTGCTGCTGCT 1462
 1222 CAGGATGGCTGGGCTCTCTGTCGCCGGCCCGAGGGGTAGCCATGCTGGGTGCTTC 1281
 1463 AAGGACTTCTCTGGTTTTTCTCCAAGAGATTCAAATCTGCTGCCATGTTAGCTGCTTT 1522
 1282 CTGCTCTCGGAGTGGCCCATGAGTATATCTCTGCTCTGCTGGGTCTCTCTATCCC 1341
 1523 GCTGATCTGCTGTAGTACAGGATATGCTGCTGGCTGTTGCTGAGCTTTTCTATCCC 1582
 1342 GTCATGCTGATCTCTCTCTGTCATTTGAGGAAATGTTGAACCTTCATGATGCAACGAG 1401
 1583 GTGCTCTGCTGCTCTCATGTTCTTTGGAATGGCTTCAACTTCATTTGCTCAATGATAGT 1642
 1402 CGCACCGGCCCGGATGGAAGCTGCTGATGTGACCATGCTGTTCTAGCGCAGGAATC 1461
 1643 CGGAAAAGCGAATTTGGAATGTTCTGATGGACTTCTCTTTCTTGGGCAATGAGGAGC 1702
 1462 CAGGTACGCTGTACTGCAAGGATGTTAGCACGGGGCACTGCCCTTTACCCCAAGCA 1521
 1703 TTACTCTGCTTTTATTTCTCAAGATGTTAGCAGTCTGACGCTGCTCTGAAATATCCC 1762
 1522 ACTTCTGGGGCTGGTGACACCTCGATCTGTTGGTCTGCGCAT 1563
 1763 ACAATTTTGGATTATGTCGGGCCACGTTCTCTGGACTTGTGT 1804

RESULT 15
 PCT-US02-21664-109
 ; Sequence 109, Application PC/TUS0221664
 ; GENERAL INFORMATION:
 ; APPLICANT: Oligos Etc., Inc.
 ; APPLICANT: DALE, Roderic M. K.
 ; APPLICANT: ARROW, Amy
 ; APPLICANT: THOMPSON, Terry
 ; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And
 ; TITLE OF INVENTION: Their Use
 ; FILE REFERENCE: 54800-5019W0

Query	Match	25.9%;	Score	405.6;	DB 1;	Length	2729;
Best Local Similarity	58.9%;	Pred. No.	7.6e-80;				
Matches	767;	Conservative	0;	Mismatches	509;	Indels	26;
Gaps							
Qy	287	CATCCCTGGGGAACAGAGAACTTTTTCATCATCCGCAAGCTCCCTGTTGATGAGCTGATGG	346				
Db	484	CACCTCCAGAACAGGAAGATTTTATGAGGCGCTCTCTTATGATGACACTGCTTG	543				
Qy	347	AGGTGCAGCATTTCCGCACCATCTACCACTATGTTTCATCGCTGGCTGTGTGTTTCATCA	406				
Db	544	AAGTGGACCACATCAGAACATATATACATGTTTATTGGCCCTCCTCATCTCTTTTATCC	603				
Qy	407	TCAGCACCTTGGCCATGCACTTCATGATGAGGCGAGCTGCTGCTGGAGTTTGACCTAC	466				
Db	604	TCAGCACACTTGTATGATACATGATGATGAGGAAGGCTGTGCTTGTAGTTACGCTCC	663				
Qy	467	TCATCTTCAGCTTCGAGACAGCTGCCATTGGCGCTGGTGAACCTGGTGGTGGCCATGTTCTGT	526				
Db	664	TGCTATGCTTTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATCATGTTCTCTGT	723				
Qy	527	CCACCCTGTGGCGCGTACACAGGCCCTACGGCTGTGGCCAGGCGCACCTGGAGCAGG	586				
Db	724	CTACATTTTCAGTTCCCTATTTCCTTTCACATTTGGGCCACTGCTATAGACAGATT	783				
Qy	587	CGACGGCGCTGGCTGTGGCTTTTAGCGCCGACGCGCTGGTGTGCTGCGCGCTGCCGG	646				
Db	784	CTCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG	843				
Qy	647	TCG-----ACGTGGCGGTGGAGCATCAGCTCCGCGCGGCTCCCGTT	688				
Db	844	TTCTAGGTTTGGACCAACATATGTTGTATTAGCATATACATGCGCACAGCTTCCCGGT	903				
Qy	689	GTGCTCTGTCTTCGAGCAGGTTAGTGTCTGATGAAAAGCTACTCCTTCTCTGAGAGAG	748				
Db	904	TCATCATTTATTCGAGCAGATTCGTTTTGTATGAGGCCCACTCATTTGTTCAGAGAGA	963				
Qy	749	CTGTGCTGGATTCCTTCGTCCGACAGAGGTGAGGGGATCCAGGCCCGCCAGTTTCTCCA	808				
Db	964	ACGTGCGCTCGGTACTTAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACA	1022				
Qy	809	G-----CTACCTCTACTTCTCTTCTGCCCACAACTCATCTACAGGGAGCTTACCCT	861				
Db	1023	GTCAAGCAGTATTGTTACTTCTTATTGTTCTTACCTTATCTACCGTGACAGCTATCCC	1082				
Qy	862	AGCAGCCCTATGTCAGGTGGAAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGT	921				
Db	1083	AGGAATCCCACTGTAAGATGGGGTATGCGCTATGAGTTTCACAGAGCTTTGGTTGC	1142				
Qy	922	GTGCTCTATGCCCTGCTTCATCCTGGGCGGCTCTGTGTTCCGTCTTGTCCACATGAGC	981				
Db	1143	TTTTTCTATGTGACTACATCTTTGAAAGGCTTTGCCCCCTTGTTCGGAATATACAA	1202				
Qy	982	CGAGAGCCCTTCAGCACCCGTCCTGCTCTCTATCTCTGATGCCAGCTTGCAGGC	1041				
Db	1203	CAGGAGCCCTTCAGCGCTCGGTGTTCTGGTCTCTATGTTTACTCCATCTTGCAGGT	1262				
Qy	1042	ATCTTTCATGCTGCTGCTCATCTTTTGGCCCTTCCTCATTTGCTGGCTCAAGCCCTTTGCC	1101				

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:20:11 ; Search time 521 Seconds
(without alignments)

US-09-918-026A-3
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 Perfect score:
 Sequence: 1 atgaagccagacggagccca.....cttgatcctgccataccctag 1569

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6062914 seqs, 2318460206 residues

Total number of hits satisfying chosen parameters: 12125828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
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8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1566.2	99.8	1983	11	US-60-452-680-12201	Sequence 12201, A
2	1566.2	99.8	1983	11	US-60-453-135-7616	Sequence 7616, Ap
3	1566.2	99.8	1983	11	US-60-453-050-7616	Sequence 7616, Ap
4	1564.2	99.7	1569	7	US-09-949-016-5159	Sequence 5159, Ap
5	1564.2	99.7	1983	8	US-10-170-235-23912	Sequence 23912, A
6	1113.4	71.0	1607	9	US-10-144-771-5649	Sequence 5649, Ap
7	421.4	26.9	2924	9	US-10-144-771-10898	Sequence 10898, A
8	407.2	26.0	4011	9	US-10-342-887-388	Sequence 388, App
9	407.2	26.0	4011	11	US-60-440-068-313	Sequence 313, App
10	405.6	25.9	2738	8	US-10-170-235-25116	Sequence 25116, A
11	405.6	25.9	2738	10	US-60-455-444-2252	Sequence 2252, Ap
12	405.6	25.9	2738	11	US-60-452-680-8056	Sequence 8056, Ap
13	405.6	25.9	2738	11	US-60-453-135-4736	Sequence 4736, Ap
14	405.6	25.9	2738	11	US-60-453-050-4736	Sequence 4736, Ap
15	345.2	22.0	508	6	US-09-532-315B-1168	Sequence 1168, Ap
16	268.2	17.1	24553	7	US-09-949-016-16901	Sequence 16901, A
17	253.4	16.2	531	8	US-10-375-682-406	Sequence 406, App
18	200.6	12.8	201	11	US-60-452-680-115000	Sequence 115000,
19	200.6	12.8	201	11	US-60-452-680-115001	Sequence 115001,
20	200.6	12.8	201	11	US-60-452-680-115003	Sequence 115003,
21	200.6	12.8	201	11	US-60-452-680-115004	Sequence 115004,
22	200.6	12.8	201	11	US-60-452-680-115005	Sequence 115005,

RESULT 1

RESOL 1
US-60-452-680-12201

; Sequence 12201, Application US/60452680

; GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: GRUPE, Andrew

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001450

; CURRENT APPLICATION NUMBER: US/60/452,680

; CURRENT FILING DATE: 2003-03-07
 ; NUMBER OF SEC TO NOS: 116212

; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FASTSEQ for Windows

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12201

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; SEQ ID NO 12201
; LENGTH: 1983

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LENGTH: 1983
TYPE: DNA

TYPE: DNA
ORGANISM: Homo sapiens

; ORGANISM: Homo sapiens
US-60-452-680-12201

T0727T-080-2C4-00-50

Query Match	99.8%	Score 1566.2	DB 11	Length 1983
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1562	Conservative	7	Mismatches	0
			Indels	0
			Gaps	0

Qy	1	ATG	GAGCAGCGGGGCCCTCTCTGCGTCTCAGAGGACAGAAAGGCTTGGAGGGGAGCGG	60
Db	1	ATG	GAGCAGCGGGGCCCTCTCTGCGTCTCAGAGGACAGRAGGGCTTGGAGGGGAGCGG	60
Qy	61	GAGCGCCAA	CCCTGTGTGAGATGGAACTCTGAGCCGACAGACCCCGGACCTTGGTACAA	120
Db	61	GAGCGCCAA	CCCTGTGTGAGATGGAACTCTGAGCGCACAGACCCCGGACCTTGGTACAA	120
Qy	121	TGGACCCGACAT	TGGAGGCTGTGAAGGCACAAATTGCTGGAGCAAGCGCAGGACACAACCTG	180
Db	121	TGGACCCGACAT	TGGAGGCTGTGAAGGCACAAATTGCTGGAGCAAGCGCAGGACACAACCTG	180
Qy	181	AGGAGCTGCT	TGGATCGGGCCATGCGGGAGGCTATACATCTTACCCATCACAGACAAA	240
Db	181	AGGAGCTGCT	TGGATCGGGCCATGCGGGAGGCTATACATCTTACCCATCACAGACAAA	240
Qy	241	CCTCTGCC	CCCCACCTCCCGAGGTTCCCTTGTGAGCAGGACCCAGAGCCATCCCTGGGGAAA	300
Db	241	CCTCTGCC	CCCCACCTCCCGAGGTTCCCTTGTGAGCAGGACCCAGAGCCATCCCTGGGGAAA	300
Qy	301	CAGAAAGT	TTTTTCATCCGCAAGTCCCTCTTGTATGAGCTGATGGAGGTGCAGCATTTTC	360


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QY 541 CCGTACCAGGCCCTACGGCTGTGGCCACAGGGCACTTGCACAGCGACGGCCCTGGGC 600
Db 541 CCGTACCAGGCCCTACGGCTGTGGCCACAGGGCACTTGCACAGCGACGGCCCTGGGC 600
QY 601 TGTGGCTTTTAGCGCCACGCCCTGGTGTCTGTGGCGCTCCGGTCCACCTGGCCGTG 660
Db 601 TGTGGCTTTTAGCGCCACGCCCTGGTGTCTGTGGCGCTCCGGTCCACCTGGCCGTG 660
QY 661 GAGCATCAGCTCCCGCGCCCTCCGTTGTGCTGTGCTTTCGACGAGTTAGTTCCGTG 720
Db 661 GAGCATCAGCTCCCGCGCCCTCCGTTGTGCTGTGCTTTCGACGAGTTAGTTCCGTG 720
QY 721 ATGAAAGCTACTCTCTCTAGAGAGGCTGTGCTGGGATCTCTCTGTCGCCAGAGGT 780
Db 721 ATGAAAGCTACTCTCTCTAGAGAGGCTGTGCTGGGATCTCTCTGTCGCCAGAGGT 780
QY 781 GAGGGATCCAGGCCCTCCAGTTTCTCCAGCTACCTCTACTTCTCTTCTGCCCAACATC 840
Db 781 GAGGGATCCAGGCCCTCCAGTTTCTCCAGCTACCTCTACTTCTCTTCTGCCCAACATC 840
QY 841 ATCTACAGGAGACTTACCCTAGGAGCCCTATGTCAAGTGAATATGTGGCCCAAGAAC 900
Db 841 ATCTACAGGAGACTTACCCTAGGAGCCCTATGTCAAGTGAATATGTGGCCCAAGAAC 900
QY 901 TTTGCCAGGCCCTGGGATGTGTCTATGCTCTATGCTCTTCACTGCGGCCCTCTGTGTT 960
Db 901 TTTGCCAGGCCCTGGGATGTGTCTATGCTCTTCACTGCGGCCCTCTGTGTT 960
QY 961 CTTGTCTTTGGCAACATGAGCCGAGAGCCCTTCAGCACCCTGGCTGTCTCTATC 1020
Db 961 CTTGTCTTTGGCAACATGAGCCGAGAGCCCTTCAGCACCCTGGCTGTCTCTATC 1020
QY 1021 CTGCATGCCACCTTGGCAGGCACTTTCATGCTGCTCATCTCTCTTTCCTTCTCCAT 1080
Db 1021 CTGCATGCCACCTTGGCAGGCACTTTCATGCTGCTCATCTCTCTTTCCTTCTCCAT 1080
QY 1081 TGTGCTCAAGCCCTTTTGGCAGATGTCTACGATTTGGAGACAGGATGTTTACCGGGAC 1140
Db 1081 TGTGCTCAAGCCCTTTTGGCAGATGTCTACGATTTGGAGACAGGATGTTTACCGGGAC 1140
QY 1141 TGGTGAAGTCAACGCTCTCTCCAACTACTACCGCACTTGAACGTGGTGTCCATGAC 1200
Db 1141 TGGTGAAGTCAACGCTCTCTCCAACTACTACCGCACTTGAACGTGGTGTCCATGAC 1200
QY 1201 TGGCTGTACAGCTACGCTGTATCAGGATGGCTGCGGCTCTTGGTCCCGGCCGAGGG 1260
Db 1201 TGGCTGTACAGCTACGCTGTATCAGGATGGCTGCGGCTCTTGGTCCCGGCCGAGGG 1260
QY 1261 GTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCATGATATCTTCTGCTTC 1320
Db 1261 GTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCATGATATCTTCTGCTTC 1320
QY 1321 GTCCCTGGGTTCTTATCCCTCATGCTGATCTCTCTGCTATTTGGAGGAATGTTG 1380
Db 1321 GTCCCTGGGTTCTTATCCCTCATGCTGATCTCTCTGCTATTTGGAGGAATGTTG 1380
QY 1381 AACTTCATGATGATGACAGCCAGCCCGGCGGATGGAAGCTGCTGATGTGGACCATG 1440
Db 1381 AACTTCATGATGATGACAGCCAGCCCGGCGGATGGAAGCTGCTGATGTGGACCATG 1440
QY 1441 CTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCAGAGTGGTACGACGGCGG 1500
Db 1441 CTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCAGAGTGGTACGACGGCGG 1500
QY 1501 CACTGCCCTTACCCAGGCACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTCTG 1560
Db 1501 CACTGCCCTTACCCAGGCACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTCTG 1560
QY 1561 CATACCTAG 1569
Db 1561 CATACCTAG 1569
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RESULT 3
US-60-453-050-7616
; Sequence 7616, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; NUMBER OF SEQ ID NOS: 2003-03-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7616
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-050-7616

Query Match 99.8%; Score 1566.2; DB 11; Length 1983;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1562; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCCAGCGGGCGCCGCTCTGCGTCTGCGAGAGACAGAAAGGCTGGAGGGGAGCGG 60
Db 1 ATGGAGCCAGCGGGCGCCGCTCTGCGTCTGCGAGAGACAGAAAGGCTGGAGGGGAGCGG 60
QY 61 GAGCCCAACCCCTGTGGAGATGAAACACTGAGACGACAGAGCCCGGACCTTGGTACAA 120
Db 61 GAGCCCAACCCCTGTGGAGATGAAACACTGAGACGACAGAGCCCGGACCTTGGTACAA 120
QY 121 TGGACCCGACACATGAGGCTGTGAAGGCACAATTTGCTGGAGCAGCGGAGGACAACTG 180
Db 121 TGGACCCGACACATGAGGCTGTGAAGGCACAATTTGCTGGAGCAGCGGAGGACAACTG 180
QY 181 AGGAGCTCTGATGTCGGGCCATGCGGGAGGCTATACAATCTTACCCTACCAAGACAA 240
Db 181 AGGAGCTCTGATGTCGGGCCATGCGGGAGGCTATACAATCTTACCCTACCAAGACAA 240
QY 241 CCTCTGCCCCACCTCCCGCAGGTTCTTGGAGCAGCAGGAGCCATCCCTGGGAAA 300
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QY 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGAGCATTTTC 360
Db 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGAGCATTTTC 360
QY 361 CGCAGCATACCATGTTTCATCGCTGCGCTGTGTCTTTCATCATGACGACCTTGCGC 420
Db 361 CGCAGCATACCATGTTTCATCGCTGCGCTGTGTCTTTCATCATGACGACCTTGCGC 420
QY 421 ATCGACTTTCATTCATGAGGCGAGGCTGCTGCTGGAGTTTGACTACTGATCTTACGTTTC 480
Db 421 ATCGACTTTCATTCATGAGGCGAGGCTGCTGCTGGAGTTTGACTACTGATCTTACGTTTC 480
QY 481 GGACAGCTGCCATTTGCGCTGTGTGACCTGGGTGCCCATGTTTCTGTCCACCTTGTGGCG 540
Db 481 GGACAGCTGCCATTTGCGCTGTGTGACCTGGGTGCCCATGTTTCTGTCCACCTTGTGGCG 540
QY 541 CGGTACCGGCCCTACGGCTGTGGGCCAGGGGACCTTGGACGAGCGGAGGCGCTTGCGC 600
Db 541 CGGTACCGGCCCTACGGCTGTGGGCCAGGGGACCTTGGACGAGCGGAGGCGCTTGCGC 600
QY 601 TGTGGCTTTTAGCGCCACGCCCTGCTGCTGCGCTGCTGCTGCGCTGCGCTGCGCTG 660
Db 601 TGTGGCTTTTAGCGCCACGCCCTGCTGCTGCGCTGCTGCTGCGCTGCGCTGCGCTG 660
QY 661 GAGCATCAGCTCCCGCGGCCCTCCCGTGTGTCTTGTCTTTCGAGCAGGTTAGTTCCTG 720
Db 661 GAGCATCAGCTCCCGCGGCCCTCCCGTGTGTCTTGTCTTTCGAGCAGGTTAGTTCCTG 720
QY 721 ATGAAAGCTACTCTCTTCTGAGAGGCTGTGCTGGGATCTCTCTTCTGCCCAACATC 780
Db 721 ATGAAAGCTACTCTCTTCTGAGAGGCTGTGCTGGGATCTCTCTTCTGCCCAACATC 780
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PRIORITY APPLICATION NUMBER: 60/231,498		PRIOR FILING DATE: 2000-09-08		NUMBER OF SEQ ID NOS: 207012		SOFTWARE: FastSeq for Windows Version 4.0		SEQ ID NO 5159		LENGTH: 1569		TYPE: DNA		ORGANISM: Human		US-09-949-016-5159																																																																																																							
Query Match		99.7%		Score 1564.2;		DB 7;		Length 1569;		Best Local Similarity		99.8%;		Pred. No. 0;		Matches 1566;		Conservative 0;		Mismatches 3;		Indels 0;		Gaps 0;																																																																																															
QY	1	ATGGAGCCAGGCGGCGCCGCTCTGCGTCTGCAGAGCAGAGAGGCTGGGAGGAGCGG	60	DB	1	ATGGAGCCAGGCGGCGCCGCTCTGCGTCTGCAGAGCAGAGAGGCTGGGAGGAGCGG	60	QY	61	GAGCGCAACCTGTGGAGATGGAACACTGAGACGCACAGAGCCCGGACTTGTGTACAA	120	DB	61	GAGCGCAACCTGTGGAGATGGAACACTGAGACGCACAGAGCCCGGACTTGTGTACAA	120	QY	121	TGAGCCCGACACATGAGGCTGTGAAGGCACAAATGCTGGAGCAAGCGCAGGAGCAACTG	180	DB	121	TGAGCCCGACACATGAGGCTGTGAAGGCACAAATGCTGGAGCAAGCGCAGGAGCAACTG	180	QY	181	AGGAGCTGCTGGATGCGGCGCATGCGGAGGCTATACAAATCTACCATCACAACACAA	240	DB	181	AGGAGCTGCTGGATGCGGCGCATGCGGAGGCTATACAAATCTACCATCACAACACAA	240	QY	241	CTCTGCCCGCCACCTCCCGAGTTCTTGGACGAGCAGGAGCCATCCCTGGGGA	300	DB	241	CTCTGCCCGCCACCTCCCGAGTTCTTGGACGAGCAGGAGCCATCCCTGGGGA	300	QY	301	CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTAGTACGCTGATGAGGTGAGCAATTC	360	DB	301	CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTAGTACGCTGATGAGGTGAGCAATTC	360	QY	361	CGACCATCTACACATGTTTCATCGCTGGCTGTCTTTCATCATCAGCAGCCCTGGGC	420	DB	361	CGACCATCTACACATGTTTCATCGCTGGCTGTCTTTCATCATCAGCAGCCCTGGGC	420	QY	421	ATGACATTCATTGATGAGGCGAGCTGCTGCTGAGTGTGACCTACTGATCTTACGCTTC	480	DB	421	ATGACATTCATTGATGAGGCGAGCTGCTGCTGAGTGTGACCTACTGATCTTACGCTTC	480	QY	481	GGACAGCTGCCATTTGGCGCTGGTGACCTGGGTGCCATGTTTCTGTCCACCTGTTGGCG	540	DB	481	GGACAGCTGCCATTTGGCGCTGGTGACCTGGGTGCCATGTTTCTGTCCACCTGTTGGCG	540	QY	541	CCGTACACAGCCCTACCGCTGTGGGCGAGGCGACCTGGAGCGAGCGGCGCTGGGC	600	DB	541	CCGTACACAGCCCTACCGCTGTGGGCGAGGCGACCTGGAGCGAGCGGCGCTGGGC	600	QY	601	TGTGCGCTTTTAGCGCGCCACGCGTGTGCTGTGCGCGTGGCGGTCCAGTGGCGGTG	660	DB	601	TGTGCGCTTTTAGCGCGCCACGCGTGTGCTGTGCGCGTGGCGGTCCAGTGGCGGTG	660	QY	661	GAGCATCAGTCCCGCGGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720	DB	661	GAGCATCAGTCCCGCGGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720	QY	721	ATGAAAAGTACTCTCTCTGAGAGGCTGTGCTGGGATCTTCTGTCGACAGAGGT	780	DB	721	ATGAAAAGTACTCTCTCTGAGAGGCTGTGCTGGGATCTTCTGTCGACAGAGGT	780	QY	781	GAGGATTCAGGCGCCCGAGTTCTCCAGCTACCTCTACTCTCTCTCTCTCTCTCTCTCT	840	DB	781	GAGGATTCAGGCGCCCGAGTTCTCCAGCTACCTCTACTCTCTCTCTCTCTCTCTCTCT	840	QY	841	ATCTACAGGAGACTTACCTTAGGAGCGCCCTATGTCAGGTGGAATATGTGGCCAAAG	900	DB	841	ATCTACAGGAGACTTACCTTAGGAGCGCCCTATGTCAGGTGGAATATGTGGCCAAAG	900

RESULT 4

US-09-949-016-5159

Sequence 5159, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: CL001307

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949.016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

RESULT 4
US-09-949-016-5159
; Sequence 5159, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTIER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

Qy 901 TTTGCCAGGCGCTGGGATGTGCTCTATGCTGCTTCATCTCTGGGCGGCTCTGTGT 960
 Db 901 TTTGCCAGGCGCTGGGATGTGCTCTATGCTGCTTCATCTCTGGGCGGCTCTGTGT 960
 Qy 961 CCTGTCTTTGGCAACATAGAGCGGAGAGCCCTTCAGCAGCCCGTGGCTGTCTCTATC 1020
 Db 961 CCTGTCTTTGGCAACATAGAGCGGAGAGCCCTTCAGCAGCCCGTGGCTGTCTCTATC 1020
 Qy 1021 CTGATGCCAGCTTGGCCAGGATCTTCATGCTGCTGCTCATCTTCTTTGGCTTCTCCAT 1080
 Db 1021 CTGATGCCAGCTTGGCCAGGATCTTCATGCTGCTGCTCATCTTCTTTGGCTTCTCCAT 1080
 Qy 1081 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGGATGTTTACCGGGAC 1140
 Db 1081 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGGATGTTTACCGGGAC 1140
 Qy 1141 TGGTGGAACTCAACGCTTCTCTCAACTACTACCGCACTTGGAGGCTGGATCATGAC 1200
 Db 1141 TGGTGGAACTCAACGCTTCTCTCAACTACTACCGCACTTGGAGCTGGATCATGAC 1200
 Qy 1201 TGGCTGTACAGCTACGTGTATCAGGATGGCTGGGCTTCTTGGTCCCGGCGCGAGGG 1260
 Db 1201 TGGCTGTACAGCTACGTGTATCAGGATGGCTGGGCTTCTTGGTCCCGGCGCGAGGG 1260
 Qy 1261 GTAGCCATGCTGGGTGTCTTCTGCTCCGACGTGGCCCATGAGTATATCTTCTGCTTC 1320
 Db 1261 GTAGCCATGCTGGGTGTCTTCTGCTCCGACGTGGCCCATGAGTATATCTTCTGCTTC 1320
 Qy 1321 GTCTGGGTTCTTCTATACCGCTCATGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
 Db 1321 GTCTGGGTTCTTCTATACCGCTCATGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
 Qy 1381 AACTTCATGATGATGACAGCGACCGCGCGGCGCATGGAACGTGCTGATGTGGACCATG 1440
 Db 1381 AACTTCATGATGATGACAGCGACCGCGCGGCGCATGGAACGTGCTGATGTGGACCATG 1440
 Qy 1441 CTGTTTCTAGCCAGGGAATCCAGTCAAGCTGACCTGCTACTCCAGGAGTGTACGACGGCGG 1500
 Db 1441 CTGTTTCTAGCCAGGGAATCCAGTCAAGCTGACCTGCTACTCCAGGAGTGTACGACGGCGG 1500
 Qy 1501 CACTGCCCTTACCCAGGCAACTTCTGCGGCTGCTGACACCTCGATCTTGTGCTCTGC 1560
 Db 1501 CACTGCCCTTACCCAGGCAACTTCTGCGGCTGCTGACACCTCGATCTTGTGCTCTGC 1560
 Qy 1561 CATACCTAG 1569
 Db 1561 CATACCTAG 1569

RESULT 5
 US-10-170-235-23912
 ; Sequence 23912, Application US/10170235
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
 ; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
 ; FILE REFERENCE: CL001380
 ; CURRENT APPLICATION NUMBER: US/10/170,235
 ; CURRENT FILING DATE: 2003-03-17
 ; NUMBER OF SEQ ID NOS: 42514
 ; SEQ ID NO 23912
 ; LENGTH: 1983
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-10-170-235-23912

Query Match 99.7%; Score 1564.2; DB 8; Length 1983;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAGCAGGCGGCGGCTGCTGCTGCTGAGAGCAGAGGCGCTGGAGGGGAGCGG 60
 |||||

Db 1 ATGAGCAGGCGGCGGCGGCTGCTGCTGCTGAGAGCAGAGGCGCTGGAGGGGAGCGG 60
 Qy 61 GAGCGCAACCTCTGGAGATGGAACACTGAGAGCAGACAGAGCCCGGACTTGTGTACAA 120
 Db 61 GAGCGCAACCTCTGGAGATGGAACACTGAGAGCAGACAGAGCCCGGACTTGTGTACAA 120
 Qy 121 TGGACCCGACACATGAGAGGCTGTGAAGCACAATTTGCTGGAGCAAGCGCAGGAGCAACTG 180
 Db 121 TGGACCCGACACATGAGAGGCTGTGAAGCACAATTTGCTGGAGCAAGCGCAGGAGCAACTG 180
 Qy 181 AGGAGCTGCTGGATCGGGCCATCGGGAGGCTATACAACTCTACCCATCAACAGACAA 240
 Db 181 AGGAGCTGCTGGATCGGGCCATCGGGAGGCTATACAACTCTACCCATCAACAGACAA 240
 Qy 241 CCTCTGCCCCACCTCCCGGAGTTCTTGAAGCAGAGCCAGAGGAGCCATCTCTGGGAAA 300
 Db 241 CCTCTGCCCCACCTCCCGGAGTTCTTGAAGCAGAGCCAGAGGAGCCATCTCTGGGAAA 300
 Qy 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTGATGAGCTGATGGAGGTGAGCATTTTC 360
 Db 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTGATGAGCTGATGGAGGTGAGCATTTTC 360
 Qy 361 CGCACCATCTACCATGTTTTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 361 CGCACCATCTACCATGTTTTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Qy 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Db 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Qy 481 GGACAGCTGCCATTTGGCGCTGGTGAACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG 540
 Db 481 GGACAGCTGCCATTTGGCGCTGGTGAACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG 540
 Qy 541 CCCTACAGGCGCTACGCTGTGGGCGAGGGGCACTTGAGCAGCGAGCGAGCGGCGCTGGCG 600
 Db 541 CCCTACAGGCGCTACGCTGTGGGCGAGGGGCACTTGAGCAGCGAGCGAGCGGCGCTGGCG 600
 Qy 601 TGTGCGCTTTTAGCGCGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 601 TGTGCGCTTTTAGCGCGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Qy 661 GAGCATAGCTCCCGCGGCTCCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db 661 GAGCATAGCTCCCGCGGCTCCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Qy 721 ATGAAAGCTACTCTCTCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 721 ATGAAAGCTACTCTCTCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Qy 781 GAGGGATCCAGGCGCCCGAGTTTCTCCAGCTACCTCTACTTCTCTCTGCTGCTGCTGCTGCTG 840
 Db 781 GAGGGATCCAGGCGCCCGAGTTTCTCCAGCTACCTCTACTTCTCTCTGCTGCTGCTGCTGCTG 840
 Qy 841 ATCTACAGGAGACTTACCTAGGAGCGCCCTATGTCAGGTGGAATATGTGCGCCAGAAC 900
 Db 841 ATCTACAGGAGACTTACCTAGGAGCGCCCTATGTCAGGTGGAATATGTGCGCCAGAAC 900
 Qy 901 TTTGGCCAGGCGCTGGGATGTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 901 TTTGGCCAGGCGCTGGGATGTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Qy 961 CCTGTCTTTGGCAACATAGAGCGGAGAGGCGCTTACAGCAGCGCTGGTGTCTCTATC 1020
 Db 961 CCTGTCTTTGGCAACATAGAGCGGAGAGGCGCTTACAGCAGCGCTGGTGTCTCTATC 1020
 Qy 1021 CTGATGCCAGCTTGGCCAGGATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1021 CTGATGCCAGCTTGGCCAGGATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Qy 1081 TGCTGGCTCAACGCGCTTTGGCCAGATGCTTACGATTTGGAGACAGGATGTTTACCGGGAC 1140
 Db 1081 TGCTGGCTCAACGCGCTTTGGCCAGATGCTTACGATTTGGAGACAGGATGTTTACCGGGAC 1140

1141 TGGTGAACCTCAACGTCCTTCCAACTACTACCGCACTTGAAGTGTGTCATGAC 1200
1141 TGGTGAACCTCAACGTCCTTCCAACTACTACCGCACTTGAAGTGTGTCATGAC 1200
1201 TGSCCTACAGCTACCTGTATCAGGATGGCTGCGGCTCTTGGTGCCCGGCGCGAGGG 1260
1201 TGGCTGTACAGCTACCTGTATCAGGATGGCTGCGGCTCTTGGTGCCCGGCGCGAGGG 1260
1261 GTAGCCATGCTGGGTGTGTTCTTCCGTCTCCGAGTGGGCCCATGAGTATATCTTGTCTTC 1320
1261 GTAGCCATGCTGGGTGTGTTCTTCCGTCTCCGAGTGGGCCCATGAGTATATCTTGTCTTC 1320
1321 GTCTGGGGTCTTCTATCCGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
1321 GTCTGGGGTCTTCTATCCGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
1381 AACTTCAATGATGATGACGACGACGCGCGCGCGCATGGAACGTGATGTGACCATG 1440
1381 AACTTCAATGATGATGACGACGACGCGCGCGCATGGAACGTGATGTGACCATG 1440
1441 CTGTTTCTAGCCAGGAATCCAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1441 CTGTTTCTAGCCAGGAATCCAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1501 CACTGCCCCCTTACCCAGGCAACTTCTGCGGGCTGGTGACACTCGATCTTGGTCTCTGC 1560
1501 CACTGCCCCCTTACCCAGGCAACTTCTGCGGGCTGGTGACACTCGATCTTGGTCTCTGC 1560
1561 CATACCTAG 1569
1561 CATACCTAG 1569

RESULT 6
US-10-144-771-5649
; Sequence 5649, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5649
; LENGTH: 1607
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-5649
Query Match 71.0%; Score 1113.4; DB 9; Length 1607;
Best Local Similarity 83.2%; Pred. No. 3,4e-255;
Matches 1296; Conservative 0; Mismatches 246; Indels 15; Gaps 2;
28 CTGCGAGAGACAGAGGCTGGGAGGAGCGGGAGCGGAGCGCCCAACCTGT---GGAGATGGA 84
51 CTTCTGGAGGAGAGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 110
-85 AACACTGAGACGACAGAGCGCGGACTTGGTACAAATGAGCCGACACATGAGGCTGTG 144
111 AACGCAAGACACAGGACCGGACACTTGGTGAATGGAATGGAATGGAATGGAATGGAATG 170
145 AAGGCACAAATGCTGGAGCAAGCGGAGGACAACTGAGGAGGAGCTGCTGGATCGGGCCATG 204
171 AAGACACAGCTTTCTGGAGCAAGCAGACAGAGAGTGGGAGAGCTTGGATCGGGCCCTA 230
205 CGGGAGGCTATACATCTTACCATCACAGACAACTCTGCCCGCACTCCCGCCAGGT 264
231 TGGGAGGCTATGCAAGCTTACCCCAACAAAGACAGACCTCTTCCCTCGCTGCCCGACAT 290
265 TCTTGAAGCAGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 324
291 TCTTGAAGCAGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 350

325 TCCCTGCTTGATGAGCTGATGAGGTGCAGATTTCCGCAACATCTACCAATGTTTATC 384
351 TCACCTGATGATGAGTAATGAGGTGCAACATTTCCGAACATCTACCAATGTTTATC 410
385 GCTGSCCTGTGTCTTCATCATCATCAGACACCTGCGCATCGACTTCATTGATGAGGCGAG 444
411 GCGGSCCTATGCGTCTGATCATCAGACACCTGCGCATCGACTTCATTGATGAGGCGAG 470
445 CTGCTGCTGGAGTTTGACCTACTGATCTTCGACAGCTTCGCAACATGCGCTGCTGTG 504
471 TTGATGCTGGAGTTTGACCTACTGATCTTCGACAGCTTCGCAACATGCGCTGCTGTG 530
505 ACCTGGGTGCCCATGTTTCTGTCACACCTGTTGGGCGCGTACCAGGCGCTTACGCGTGTGG 564
531 ACCTGGGTGCCCATGTTTCTGTCACGCTCTAGTGCCTTACCAGACCTTGGCTGTGG 590
565 GCGA-----GGGCGACCTGGAGCGAGCGCGCTGGGCTGTGGCTTTT 612
591 GCGAGCGCGCGCTGGGCGTGGATGCTGGGCGCGAGCTGGGCTGTGGCTGTGGCT 650
613 GCGCGCCACGCGCTGCTGCGCGCTGCGGCTCCAGCTGGCGGTGGAGCATCAGCTC 672
651 GCTGCCACGCTGTGCTGCTGCTGCTGCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
673 CGCGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
711 CGCGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
733 TCTTCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
771 TCTTCTCTGAGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
793 GCGCGCGCTTCTCCAGTACCTCTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
831 GCGCGCGCTTCTCCAGTACCTCTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
853 ACTTACCTTAGGACGCGCTTATGCTAGTGGAAATATGCGCAAGAACTTTGCCCGAGCG 912
891 ACATACCGGAGGACACCGGAGTACAGTGGAAATATGCGCAAGAACTTTGCCCGAGGTC 950
913 CTGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
951 CTGGCTGTTTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010
973 AACATGAGCGGAGCGCTTACAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
1011 AACATGAGCGGAGCGCTTACAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
1033 TTGCGAGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
1071 GCGCGAGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
1093 GCCTTTGCCAGATGCTTACGATTTGAGACAGGATGTTCTACCGGAGCTGGTGAATCTCA 1152
1131 GCCTTTGCCAGATGCTTACGATTTGAGACAGGATGTTCTACCGGAGCTGGTGAATCTCG 1190
1153 ACCTGCTTCTCCAGTACTACCGCTTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1212
1191 ACTTCTTCTCCAGTACTACCGCTTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250
1213 TACGTGTATCAGGATGGCTGCGGCTCTTGGTGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1272
1251 TATGTGTATCAAGATGGCTGTGCTTATAGGAGGCGGCTGCGGCGGCTGCGGCGGCTGCTGCTGCT 1310
1273 GGTGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
1311 GAGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
1333 TCTTATCCGCT 1392
1371 TCTTACCGGCT 1430

; LENGTH: 4011
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-388

Query Match 26.0%; Score 407.2; DB 9; Length 4011;
Best Local Similarity 59.0%; Pred. No. 9.2e-87;
Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;

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QY 287 CATCCCTGGGGAACAAAGATTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTGATGG 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1737 CACCTCCAGAACAGGAAAGATTTTATGCAAGGGCGCTCTCTCTAGATGAACCTGTTG 1796

QY 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1797 AAGTGGACACATCAGAACATATATACATGTTTATGCGCTCCCTCATCTCTTATCC 1856

QY 407 TCAGACCCCTGGCCGATCGACTTCATGATGAGGCGAGCTGTGCTGGAGTTTGACCTAC 466
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1857 TCAGACACATGTAGTAGATTACATGATGAAAGGCTGTGCTGATGAGCTCAGCCTCC 1916

QY 467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGTGTGAGCTGGGTGCCCATGTTTCTGT 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1917 TGTCTTAGCTTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATCATGTTCTGT 1976

QY 527 CCACCCTGTTGGCCGCTACAGGCCCTACGGCTGTGGGCCAGGGGCACTTGGACGAGG 586
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1977 CTACATTTTTCAGTTCCCTATTTCTGTTCAACATTTGGGCACTGGCTATAGCAAGATT 2036

QY 587 CGAGGGCGCTGGCTGTGCGCTTTTACGCCCCACGCGGTGGTCTCTGCGCGTGCGGG 646
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2037 CTATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTCATCATGATCTTCCAGATTGGAG 2096

QY 647 TCC-----ACGTGGCGGTGGAGCATGAGCTCCCGCGCGCTCCCGTT 688
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2097 TTTAGGTTTTGGACCAACATATGTTGTTAGCATATACATGCCACGAGTTCCCGGT 2156

QY 689 GTGCTCGCTGTGAGGAGTTAGTTCTCTGATGAAAGCTACTCTCTTCTGTAGAGAGG 748
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2157 TCATCATATATTCGAGCAGATTCGTTTGTGTAAGAGGCCACTCATTTGTCAAGAGA 2216

QY 749 CTGTCCTGGGATCCTTCGTCAGAGAGGTGAGGATCCAGGCCCTCCAGTTCCTCCA 808
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2217 AGTGCTTCGGGTACTAAAT-TCAGCTAAGAGAAATCAAGCACTGTTCNAATACCTACA 2275

QY 809 G-----CTACCTCTACTCTCTTTCGCCCAACACTCATCTACAGGAGACTTACCT 861
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2276 GTCAACCAAGTATTTGACTTCTTATTTGCTCTTACCTTATCTACCGGTGACAGCTATCC 2335

QY 862 AGGAGCCCTATGTGAGTGAATATGTGCGCAAGAACTTTGCCAGGCCCTGGATGT 921
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2336 AGGAATCCCACTGTAAAGATGGGTATGTCGCTATGAAGTTTGGACAGGTCTTTGGTTGC 2395

QY 922 GTGCTCTATGCTGCTTCATCTGCGCGCGCTCTGTGTTCTCTGCTTTCGCAACATGAGC 981
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2396 TTTTCTATGTGACTACATCTTTGAAGGCTTTGTGCGCCCTGTTTCGGAATATCAAA 2455

QY 982 CGAGAGCCCTTCAGACCCGCTGCTGTCTCTATCTGCAATGCCACGCTTGCAGGC 1041
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2456 CAGGAGCCCTTCAGGCTCGTGTGCTGCTCTATGATGATTTAACTCCATCTTCCAGGT 2515

QY 1042 ATCTTCATGCTGCTGCTCATCTCTTTCCTTCCATGCTGTGCTCAAGCCCTTTGCC 1101
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2516 GTGCTGATCTCTCTTACTTCTTTTTCCTTTTGGCTTTTGGCTGCTGCTCAATGCTTGTCT 2575

QY 1102 GAGATGCTACGATTTGGAGACAGGATGTTTACCGGAGTGGTGGAACTCAACGCTCTTC 1161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGTGAACCTCCACGCTATAC 2635

QY 1162 TCCAACTACTACCGACTTGGAACTGGTGGTCCATGACTGCTCTACAGTACCTGAT 1221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2636 TCCAACTATTATAGAACCTGGAATGTTGGTCCATGATGACTGGCTATATTACTATGCTTAC 2695
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RESULT 9

US-60-440-068-313
; Sequence 313, Application US/60440068
; GENERAL INFORMATION:

; APPLICANT: CARMAN, STEVEN G.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
; TITLE OF INVENTION: NF-KB PATHWAY
; FILE REFERENCE: 3053-4191
; CURRENT APPLICATION NUMBER: US/60/440,068
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 313
; LENGTH: 4011
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-440-068-313

Query Match 26.0%; Score 407.2; DB 11; Length 4011;

Best Local Similarity 59.0%; Pred. No. 9.2e-87;
Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;

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QY 287 CATCCCTGGGGAACAAAGATTTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTGATGG 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1737 CACCTCCAGAACAGGAAAGATTTTATGCAAGGGCGCTCTCTCTAGATGAACCTGTTG 1796

QY 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1797 AAGTGGACACATCAGAACATATATACATGTTTATGCGCTCCCTCATCTCTTTATCC 1856

QY 407 TCAGACCCCTGGCCGATCGACTTCATGATGAGGCGAGCTGTGCTGGAGTTTGACCTAC 466
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1857 TCAGACACATGTAGTAGATTACATGATGAAAGGCTGTGCTGATGAGCTCAGCCTCC 1916

QY 467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGTGTGAGCTGGGTGCCCATGTTTCTGT 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1917 TGTCTTAGCTTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATCATGTTCTGT 1976

QY 527 CCACCCTGTTGGCCGCTACAGGCCCTACGGCTGTGGGCCAGGGGCACTTGGACGAGG 586
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1977 CTACATTTTTCAGTTCCCTATTTCTGTTCAACATTTGGGCACTGGCTATAGCAAGATT 2036

QY 587 CGAGGGCGCTGGCTGTGCGCTTTTACGCCCCACGCGGTGGTCTCTGCGCGTGCGCG 646
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2037 CTATCCGCTGATCCGTTCTCTCTTCCATGAGCTTTCTTTCATCATGATCTTCCAGATTGGAG 2096

QY 647 TCC-----ACGTGGCGGTGGAGCATGAGCTCCCGCGCGCTCCCGTT 688
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||||| 1396 TCAACTATTATAGAACCTGGAAATGTTGGTCCATGACTGGCTATATTACTATGCTTAC 1455
QY 1222 CAGGATGGGCTGGCTCTTGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTC 1281
Db 1456 AAGGACTTCTCTGGTTTCTCCAGAGATTCAAATCTGCTGCCATGTAGCTGCTTT 1515
QY 1282 CTGGTCTCCGACATGGCCATGAGTATATCTTCTGCTTGGTCTGGGTCTTCTATCCC 1341
Db 1516 GCTGTATCTCTAGTACAGGAATATGCTTGGCTGTTTGGTGGCTTCTTATCCC 1575
QY 1342 GTCATGCTGATCTCTCTCTGTCATTTGGAGGAATGTTGAATTCATGATGATGACACAG 1401
Db 1576 GTGCTCTTCTGCTCTCTCTCTCTTCTTGGATGGCTTCAATTCATGTCATGATAGT 1635
QY 1402 CGACCGGCGGCGCATGGAACTGGTGTGATGTGACCATGCTGTTCTAGGCCAGGAATC 1461
Db 1636 CGGAAAAAGCCGATTTGGAATGTTCTGATGTGGACTTCTCTTCTTGGGCAATGGAGTC 1695
QY 1462 CAGGTACAGCTGTACTGCCAGGAGTGTAGCCACGGCGGCACTGCCCTTACCCAGGCA 1521
Db 1696 TTACTCTGCTTTTATCTCAAGATGATGATGACGTGACACTGTCTCTGAAAAATCCC 1755
QY 1522 ACTTCTGGGGCTGTGTGACACCTCGATCTTGGTCTGCTGCTAT 1563
Db 1756 ACATTTTGGATTATGTCGGCCACGTTCTCGGACTTGTGCT 1797

RESULT 11
US-60-455-444-2252
; Sequence 2252, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: BEGOLICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2252
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-2252

Query Match 25.98; Score 405.6; DB 10; Length 2738;
Best Local Similarity 58.98; Pred. No. 1.9e-86;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCCGCAAGTCCCTGCTGTGATGAGCTGATGG 346
Db 497 CACCTCCAGAACAGAAAGATTTTATTGAAGGCGCTCTCTCTAGATGAACCTGCTG 556
QY 347 AGGTGACAGATTTCCGACCATCTACACATGTTTCATCGCTGGCTGTGCTCTTCATCA 406
Db 557 AAGTGACCATCATAGAACATATATACATGTTTATTGGCCCTCTCATCTCTTTATCC 616
QY 407 TCAGCACCTGCGCATCTCACTTCACTGATGAGGCGAGCTGCTGCTGGAGTTTGACCTAC 466
Db 617 TCAGCACACTTCTAGTATGATGATGAGGAGGCTGGTCTTGGAGTTCAGCTTCC 676
QY 467 TGATCTTCAGCTTCGACAGCTGCCATGGCGCTGGTGAACCTGGGTGCCATGTTTCTGT 526
Db 677 TGCTTATGCTTTTGCAAAATTCCTACCGTGTGTTGGACCTGGTGGATCATGTTCTGT 736
QY 527 CCACCTCTGTTGGCGCGTACACAGGCCCTACGCGCTGGGCCAGGGCCACCTGGAGCAGG 586
Db 737 CTACATTTTTCAGTTCCTATTTCTGTTTCAACATTTGGGCCACTGGCTATAGCAAGATT 796
QY 587 CGACGGCTGGCTGTGCTGCTTTTAGCGCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
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Db 797 CTCATCCGCTGATCGTTCTCTCTTCCATGCTTCTTTTCATGATCTTCAGATGAG 856
QY 647 TCC-----ACGTGGCGGTGGAGCATCAGCTCCCGCGCCCTCCCGTT 688
Db 857 TTCTAGGTTTGGACCAACATATGTTGTTAGCATATACACTGCCACAGCTTCCCGT 916
QY 689 GTGCTCCTGCTTTCGAGCAGGTTAGGTTCTCTGATGAAAGCTACTTCTCTCTGAGAGG 748
Db 917 TCATCATATATTCGAGCAGATTCGTTTGTAAAGGCCCACTCAATTGTGACAGAGA 976
QY 749 CTGTCCTGGGATCCTCGTCCAGACAGAGTGAGGGGATCCAGCCCCCAGTTCTTCCA 808
Db 977 ACGTCCCTCGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCCAATACATA 1035
QY 809 G-----CTACTCTACTTCTCTCTCTGCCCCAACACATCATACAGGAGAGCTTACCC 861
Db 1036 GTCAACCACTATTTGACTTCTTATTTGCTCCTACCCTTATCTACCGTGACAGCTATCCC 1095
QY 862 AGGAGCCCTATGTGAGGTGGAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGATGT 921
Db 1096 AGGAATCCCACTGTAAAGATGGGTTTATGCTGCTATGAAGTTTGCACAGCTCTTGGTGC 1155
QY 922 GTGCTCTATGCTCTCTCTCTGCGGCCCTCTCTGTTTCTCTCTTTTGGCCAAATGAGC 981
Db 1156 TTTTCTATGCTACTACATCTTGAAGGCTTGTGCCCCCTTGTTCGGAATATCAAA 1215
QY 982 CGAGAGCCCTTCAGACCCGCTGCCCTGTGCTCTCTATCTCTGATGCCAGCTTGCAGGC 1041
Db 1216 CAGGAGCCCTTCAGCGCTGCTCTCTGCTCTCTGTTTAACTCCATCTTGGCAGGT 1275
QY 1042 ATCTTCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1101
Db 1276 GTGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1335
QY 1102 GAGATCTACGATTTGGAGACAGAGTGTCTTACCGGGAGTGTGGAACTCAACGCTCTTC 1161
Db 1336 GAGATCTACGCTTGTGTGACAGAGTGTCTTATAAGGATTTGTGGAACTCCACGTCTAC 1395
QY 1162 TCAACTACTACCGCACTTGGAACTGTTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1221
Db 1396 TCAACTATTTATAAGAACCTGGAATGTTGGTGTCCATGCTGCTGCTGCTGCTGCTGCTG 1455
QY 1222 CAGGATGGGCTGCGCTCTCTGTTGGTGGCGGCCGAGGGGTAGCCATGCTGGGTGTTTC 1281
Db 1456 AAGGACTTCTCTGGTTTCTCCAGAGATTCAAATCTGCTGCCATGTTAGCTGCTTT 1515
QY 1282 CTGCTCTCCGAGTGGCCCCATGAGTATATCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1341
Db 1516 GCTGTATCTCTCTAGTACAGGAATATGCTTGGCTGTTTGGCTGTTTCTATCCC 1575
QY 1342 GTCATGCTGATCTCTCTCTGTCATTTGGAGGAATGTTGAATTCATGATGATGACACAG 1401
Db 1576 GTGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1635
QY 1402 CGCACCGCCCGGCGATGGAACGCTGATGTGGACCAATGCTGTTTCTAGGCCAGGAATC 1461
Db 1636 CGGAAAAAGCCGATTTGGAATGTTCTGATGGAATGCTTCACTTCACTTCACTGATGATG 1695
QY 1462 CAGGTACGCTGTACTGCCAGGAGTGTAGCCAGGGCGGCACTGCCCTTACCCAGGCA 1521
Db 1696 TTACTCTGCTTTTATCTCAAGATGTTATGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1755
QY 1522 ACTTCTGGGGCTGGTGGACACCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1563
Db 1756 ACATTTTGGATATGTCGGCCACGTTCTCTGGACTTGTGCT 1797
```

RESULT 12
US-60-452-680-8056
; Sequence 8056, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/60/452,680
; NUMBER OF SEQ ID NOS: 2003-03-07
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8056
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-8056

Query Match 25.9%; Score 405.6; DB 11; Length 2738;
Best Local Similarity 58.9%; Pred. No. 1.9e-86;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

Qy 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGAAAGTCCCTGCTGTAGTGAAGTGTATGG 346
Db 497 CACCTCCAGAAACAGGAAGATTTTATTCGAAGCGCTCTCTCTAGATGAAGTGTATGG 556
Qy 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGGCTGTGTCTCTATCA 406
Db 557 AAGTGGACCATCAGAACATATACATGTTTATTCGCTCTCTCTCTATTCCTTATCC 616
Qy 407 TCAGCACCTTGGCCATCGACTTCATGATGAGGAGGCTGCTGTGGAGTTTGACCTTAC 466
Db 617 TCAGCACCTTGTAGTAGTATGATGAGGAGGCTGCTGTGGAGTTTGACCTTAC 576
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGTGACCTGGTGGTCCCTTCTGT 526
Db 677 TGCTTATGCTTTTGGCAATTTCTACCGTGTGTGGACCTGGTGGATCATGTTCTCGT 736
Qy 527 CCACCTCTTGGCCCGTACAGGCCCTACGGCTGTGGCGGACGGGACCTTGGAGCAGG 586
Db 737 CTACATTTTCAGTTCCTCTATTTCTGTTTCAACATTTGGGCGACCTTGGCTATAGCAAG 796
Qy 587 CGAGGGGCTGGGTGTGCGCTTTTAGCGCGCCACGCGTGTGCTCTCGCGCTGTCCGG 646
Db 797 CTCATCGCTGATCGTCTCTCTTCCATGCTTTTCTTTCATGATCTTCCAGATTTGAG 856
Qy 647 TCC-----ACGTGGCGGTGAGCATCATCAGCTCCGCGCGCTCCCGTT 688
Db 857 TTCTAGGTTTTGGACCAACATATCTGTGTAGCATATACATCCACAGCTTCCCGGT 916
Qy 689 GTGCTCTGCTTCGAGCAGGTTAGTGTCTGATGAAAGCTACTCTCTCTGAGAGAGG 748
Db 917 TCATCATATATTCGACGAGATTCGTTTGTATGAAGGCCCACTCATTTGTCAGAGAGA 976
Qy 749 CTGTGCTTGGGATCTTGTGTCAGAGAGGATGAGGGGATCCAGGCCCTCCAGTTTCTCCA 808
Db 977 ACGTGCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTTCCAATACCTACA 1035
Qy 809 G-----CTACCTCTACTCTCTCTGCGCCACACATCATCTACAGGAGACTTACCT 861
Db 1036 GTCAACAGCAATTTGTACTTTTATTTGCTCTTACCTTATCTACCGGTGACAGCTATCC 1095
Qy 862 AGGAGGCCCTATGTCAGTGAATATGTCGCAAGAACTTTGCCAGGCCCTGGAGGT 921
Db 1096 AGGAATCCCACTGTAAAGTGGGTATGTCGCTATGAAGTTTGCACAGGTTCTTGGTTGC 1155
Qy 922 GTGCTCTATGCTCTCATCTGGGCGCTCTGTGTCTGTCTGTCTGTTGCCAAGATGAGC 981
Db 1156 TTTTCTATGTACTACATCTTTGAAAGGCTTTGTGCGCCCTTGTTCGGAATATCAAA 1215
Qy 982 CGAGAGCCCTTCAGACCCGTGGCTGTCTCTATCTCTGATGCAAGCTTGTCCAGGC 1041
Db 1216 CAGGAGCCCTTCAGCGCTCGTGTCTCTGCTCTATGTTTAACTTCACTTCCAGGT 1275
Qy 1042 ATCTTCATGCTGCTCATCTTCTTGGCTTCTCTCCATTTGCTGCTCAAGCCCTTGGC 1101
Db 1276 GTGCTGATCTCTCTTCTTTTGGCTTTTGTGCACTGCTGGCTCAATGCTCTTGTCT 1335

RESULT 13

US-60-453-135-4736
; Sequence 4736, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4736
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-4736

Query Match 25.9%; Score 405.6; DB 11; Length 2738;
Best Local Similarity 58.9%; Pred. No. 1.9e-86;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

Qy 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTATGAGTGTATGG 346
Db 497 CACCTCCAGAACAGGAAGATTTTATTCGAAGCGCTCTCTCTTAGATGAAGTGTCTT 556
Qy 347 AGGTGACGATTTCCGCAACCATCTACCATGTTTCATCGCTGGCGTGTGTCTTTCATCA 406
Db 557 AAGTGGACCATCAGAACATATATACATGTTTATTCGCTCTCTCTCTTATCC 616
Qy 407 TCAGCACCTTGGCCATCGACTTCATGATGAGGAGGCTGCTGTGGAGTTTGACCTTAC 466
Db 617 TCAGCACCTTGTAGTAGTATGATGAGGAGGCTGCTGTGGTGTGAGTTTCAGCTCC 676
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGTGACCTGGTGGTCCCTTCTGT 526
Db 677 TGCTTATGCTTTTGGCAATTTCTACCGTGTGTGGACCTGCTGGATCATGTTCTCTGT 736
Qy 527 CCACCTCTTGGCGCGCTTACCAGGCCCTACGCTGTGGCGGACGGGACCTTGGAGCAGG 586

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